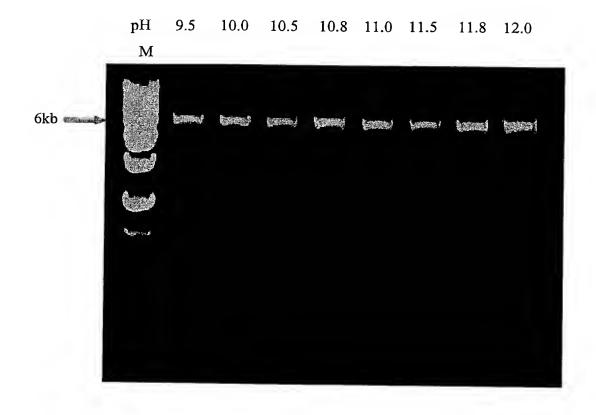
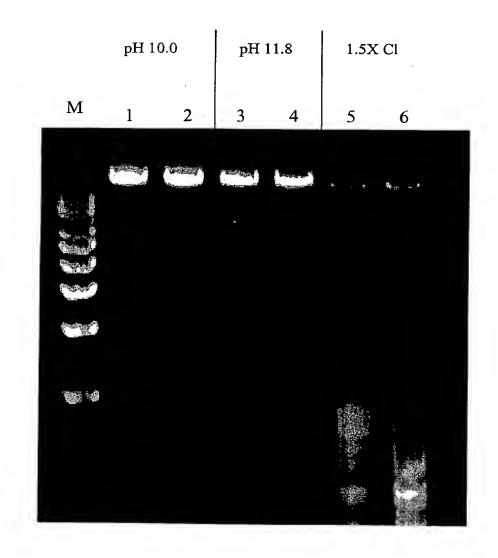
Chimeric blend A PH 5.0 7.0 7.5 8.0 8.5 9.0 9.5 10.0 5.0 7.0 7.5 8.0 8.5 9.0 9.5 10.0 M 6kb

6kb BG 15"/kb - 1'-30"

1X Cloned buffer



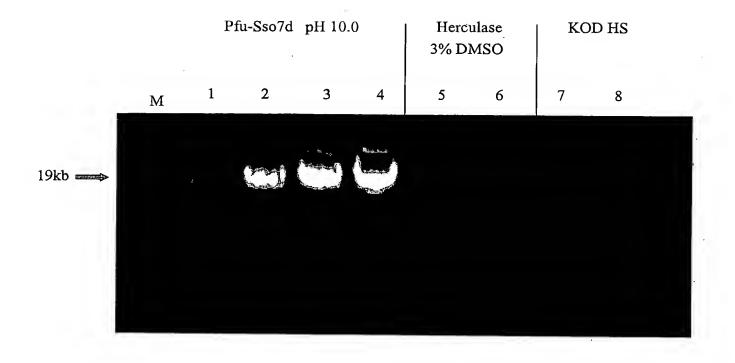
19kb BG 30"/kb - 9.5' extension



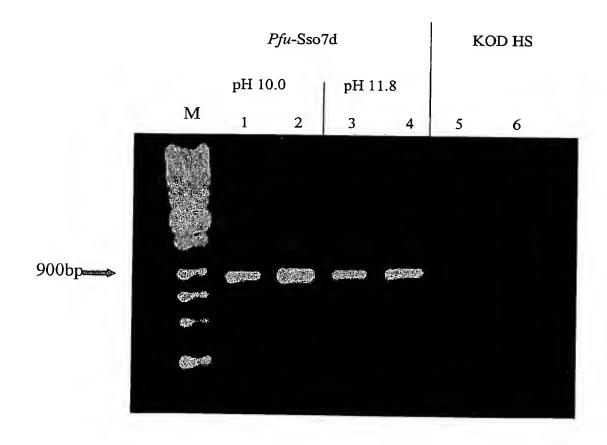
19kb BG 30"/kb - 9.5' extension

		Pfu-Sso7	7d blend [10.0		Sso7d 10.0	Hercı	ılase		culase OMSO
_	M	1	2	3	<i>t</i> 4	5	6	7	8
19kb	a) de s	養 縣 滋油	Star in P						

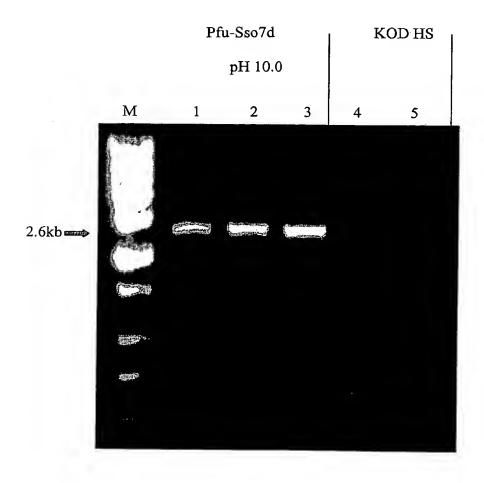
19kb BG 30"/kb - 9.5' extension



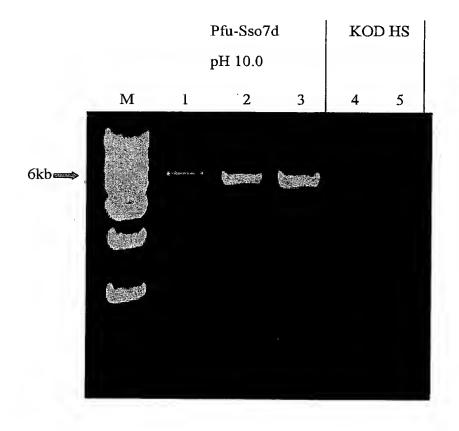
900bp HαAT 1"/kb - 1" extension



2.6kb HαAT 2"/kb - 5" extension



6kb BG 10"/kb - 1' extension



2.6kb HαAT 30"/kb - 1'. 18" extension

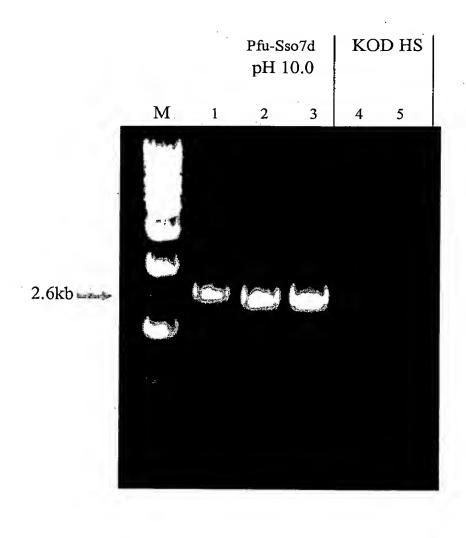


Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAgATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 5)

V93E#2

5'-CTTTTTCTCTAATAgTgggTTCATCTTgggggATgTTC-3' (SEQ ID NO: 6)

V93R#1

5'-gAACATCCCCAAgAT<u>AgA</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 7)

V93R#2

5'-CTTTTTCTCTAATAgTgggTCTATCTTgggggATgTTC-3' (SEQ ID NO: 8)

V93N#1

5'-gAACATCCCCAAgAT<u>AAC</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 9)

V93N#2

5'-CTTTTTCTCTAATAgTggggTTATCTTgggggATgTTC-3' (SEQ ID NO: 10)

V93H#1

5'-gAACATCCCCAAgAT<u>CAC</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 11)

V93H#2

5'-CTTTTTCTCTAATAgTggggTgATCTTgggggATgTTC-3' (SEQ ID NO: 12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAgATNNKCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 13)

V93K#1

5'-gAACATCCCCAAgAT<u>AAA</u>CCCACTATTAgAg-3' (SEQ ID NO: 14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 15)

QCM#1 5'-(Phosphate)gAACATCCCCAAgATgCACCCACTATTAgAgAAAAAg-(SEQ ID NO:

16)'

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAgATgACCCCACTATTAgAgAAAAAg-3'(SEQ ID

NO: 17)

Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAgATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 18)

Cysteine

QCM#4 5'-

(Phosphate)gAACATCCCCAAgATATACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 19)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAgATATgCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 20)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAgATTTCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 21)

FIGURE 10 (CONT.)

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAgATCCTCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAgATAgCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAgATACACCCACTATTAgAgAAAAAg- 3' (SEQ ID

NO: 24)

Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAgATTACCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 25)

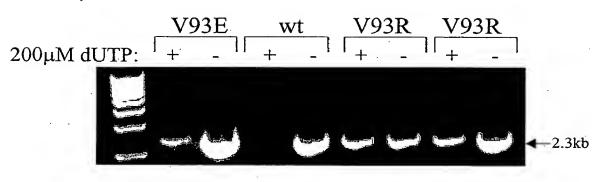
Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAgATTggCCCACTATTAgAgAAAAAg-3'

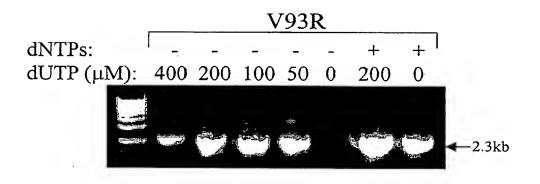
(SEQ ID NO: 26)

Tryptophan

a.)



b.)



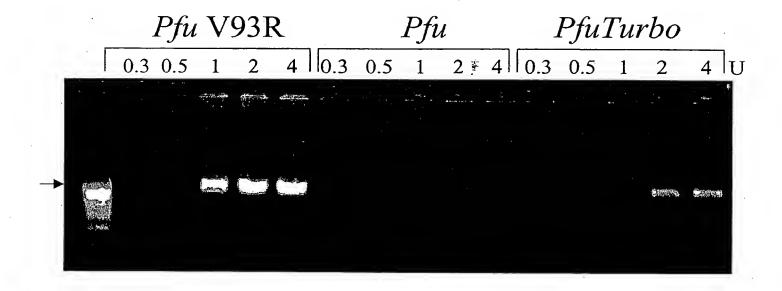


FIGURE 13A

PFU DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 28)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE

FIGURE 13A (CONT.)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T) V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 29) V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 31)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 32)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120

```
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGTG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGGTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
```

KOD DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 33)

V93R MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEO ID NO

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 34)

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACNNNC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGT GAAGTGAAG GGCAGATACA CCTTCGATCT 780

FIGURE 13A (CONT.)

```
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CTTGA 2325
Vent DNA POLYMERASE
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 35)
V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO:
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACNNNC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
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GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440 ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500

FIGURE 13A (CONT.)

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GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTAAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCCTCAAGA GGTAG 2325
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Deep Vent

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 37)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 38)

38)						
		CATCACCGAG				60
		GGTTGAGTAC				120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
		TGCCGAAAAG				240
GAGGTATGGA	GGCTGTACTT	TGAACACCCT	CAGGACNNNC	CCGCAATAAG	GGATAAGATA	300
		TGACATCTTT				360
		TCCAATGGAA				420
		CGAAGGGGAG				480
		AGCCAAAGTC				540
		GAGGGAGATG				600
		TACCTACAAC				660
		GATAAAGCTA				720
		GACAGCGGTG				780
		GATAAACCTC				840
		GGAGAAAGTT				900
		AGTTGCAAAG				960
		CCCAATGGAG				1020
		TTCAACTGGC				1080
		GGCTCCAAAC				1140
		GGGATACGTT				1200
		GAGCCTGTAC				1260
		AGGGTGTAGG				1320
		GGGGTTTATC				1380
		GATGAAAGCT				1440
		CAAAATCCTG				1500
		TAAGGAGTGC				1560
		GGAACTGGAG				1620
		CACAATTCCT				1680
		TATAAACGCC				1740
		GTTCTTCGTG				1800
		GGGGCTTGAA				1860
		CCTAGAGGCT				1920
		AACTGAAAAG				1980
		CACGAGGCCC				2040
		AGCCGCTAGA				2100
		AGACGGGCCA				2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
•						

FIGURE 13A (CONT.)

GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA 2328

JDF-3

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 39)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 40) ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGGACGCGAGTTCA GGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCCTCGGCAGGTCT GTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACNNNCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGG TCATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGA GGAAGAGCTTAAACTCATGTCCTTCGACATCGACGCCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCGATTCTG CCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGG GAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCA TAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGT CTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCG AGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGG CTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCCTTCAATCATAATCACCCACAACGTCTCGCCAGATA CATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTG GAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCA GGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGA GCTTGAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCT GAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTCGAACTCGAATACG AGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGGGGCAAGATAACCACGCG CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGG CACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGA AGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAgcG TTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGC GACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTC TGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGG GCTTGGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

Figure 13B

>Pfu V93R (SEO ID NO:41)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS //

>Pfu V93E (SEQ ID NO:42)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/G387P (SEQ ID NO:43)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/D141A/E143A(SEQ ID NO:44)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/G387P(SEQ ID NO:45)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/D141A/E143A(SEQ ID NO:46)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>DEEP VENT V93R(SEQ ID NO:47)

MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>DEEP VENT V93E(SEO ID NO:48)

MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>TGO V93R (SEQ ID NO:49)

FIGURE 13B (CONT.)

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK

>TGO V93E(SEQ ID NO:50)

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R(SEQ ID NO:51)

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E(SEQ ID NO:52)

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

FIGURE 13B (CONT.)

>VENT V93R (SEO ID NO:53)

MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E (SEQ ID NO:54)

MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R(SEQ ID NO:55)

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR SVEVWVLYFTHPQDR PAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK ATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E(SEQ ID NO:56)

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK
ATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

Figure 14

Tgo 93:

NNN = AGA, AGG, CGA, CGC, CGG, CGT (R) (NUCLEOTIDE SEQUENCE: SEQ ID NO: 57; AMINO ACID SEQUENCE: SEQ ID NO: 58) NNN = GAA, GAG (E)(NUCLEOTIDE SEQUENCE: SEQ ID NO: 59; AMINO ACID SEQUENCE: SEQ ID NO: 60) atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc 48 Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile 96 agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att 144 Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile 192 gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg 50 gtt gtc agg gcc gag aaa gtg aag aag ttc cta ggc agg ccg ata 240 Val Val Arq Ala Glu Lys Val Lys Lys Phe Leu Gly Arg Pro Ile 65 gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc 288 Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile 85 agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac 336 Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr 105 gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg 384 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg 432 Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata 480 Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile 145 150 age tac gee gae gag gaa ggg geg ege gtt att acc tgg aag aat atc 528 Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile 165 170 175 gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag 576 Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys 180

FIGURE 14 (CONT.)

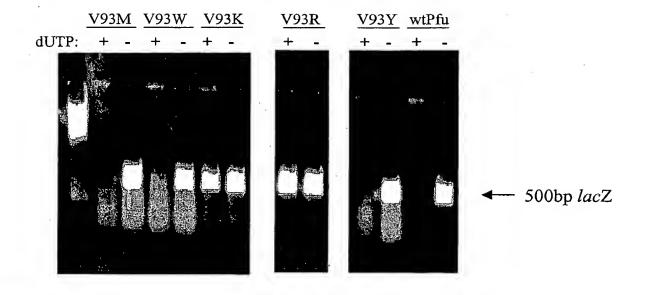
_			_	_	gtc Val	_	_	_	_		_					624
			_		ttc Phe	_		_			_	_	_			672
					ttc Phe 230											720
					gat Asp											768
		_			ccc Pro	_			_	_						816
					gta Val											864
					gag Glu											912
	_			_	cgc Arg 310		_	_		_	_	_	-			960
					ttc Phe											1008
_		_	_		tgg Trp	_	_		_	_	_					1056
					ctg Leu											1104
		_	_	_	gag Glu			_	_	_	_			_		1152
				_	aag Lys 390			_			-					1200
		_	_		cgc Arg		_			_						1248
aac	gtc	tcc	cct	gat	aca	ctc	aac	agg	gag	ggt	tgt	gag	gag	tac	gac	1296

FIGURE 14 (CONT.)

Asn	Val	Ser	Pro 420	Asp	Thr	Leu	Asn	Arg 425	Glu	Gly	Cys	Glu	Glu 430	Tyr	Asp	
					ggc Gly											1344
					gga Gly											1392
					act Thr 470											1440
			_	_	atc Ile				_		_					1488
					gcc Ala											1536
					agg Arg											1584
					ttt Phe											1632
					gga Gly 550											1680
					tac Tyr											1728
					ttc Phe											1776
					gac Asp											1824
					gac Asp											1872
					ata Ile 630											1920
					gtt Val											1968

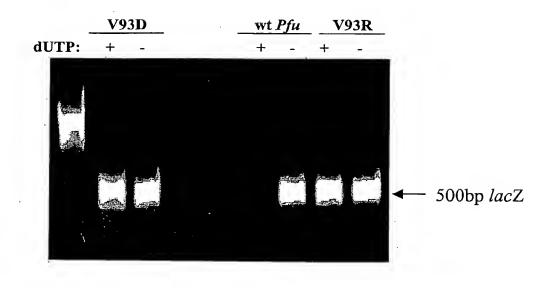
FIGURE 14 (CONT.)

	645	650	655
	Val Ile Tyr Glu G	eag ata acc cgc gac of the control of the cap is a con	
		get gtt gca aaa cgc o Ala Val Ala Lys Arg 1 685	
		acg gtc ata agc tac a Thr Val Ile Ser Tyr 1 700	
		agg gct ata ccc ttt g Arg Ala Ile Pro Phe 7 715	
		gca gaa tac tac atc o Ala Glu Tyr Tyr Ile o 730	
	Val Glu Arg Ile L	etg agg gcc ttt ggt (Leu Arg Ala Phe Gly (745	
		egg cag gtt ggc ttg g Arg Gln Val Gly Leu G 765	
cta aaa cct aag Leu Lys Pro Lys	-		2322



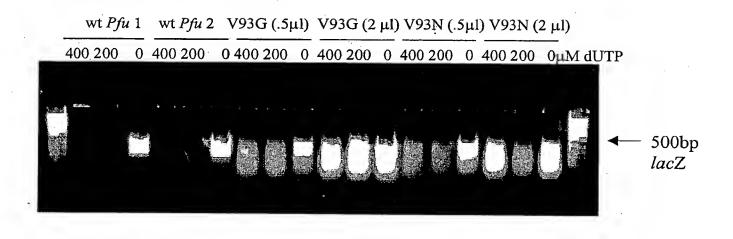
Results: *Pfu* V93K and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93W, V93Y, and V93M mutants show little-to-no improvement in dUTP incorporation.

FIGURE 15B



Results: The Pfu V93D and V93R mutants show significantly improved dUTP incorporation compared to wild type Pfu.

FIGURE 15C



Results: The *Pfu* V93N mutant shows a very small improvement in dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93G mutant shows little-to-no improvement.

Figure 16: Polymerase activity and Temperature optimum of Pfu N terminal truncation mutants

Pfu clone #	Truncated after Pfu residue	Relative DNA polymerase activity	Temperature Optimum
61	H30	Moderate	65°
72	V66	Similar to wild type	70°
81	P128	Low	Not tested
92	I158	Low	Not tested
3	G125	Similar to wild type	Not tested
13/14	K201	low	65° .

Figure 17A

			18	54	36	108	54	162	69	207
			ט	GGT	ы	GAA	ഷ	AGA		
			Ø	GCT	M	GAG	Ö	GGT		
			×	AAG	J	CTT	ø	GCA		
			æ	AGA	H	CAC	Ħ	CAC	*	TGA
<u></u>	ı		н	ATA	ы	GAG	×	AAG	တ	AGC
(HMf-11ke)			'n	CTT	4	GCA	Ø	GCA	, ×	AAG
HMÉ-			æ	AGA	П	CTT	ц	CLT	н	ATT
			Q	GAC	>	GTA	Ω	GAT	ø	GCA
histone			>	GTT	×	AAG	>	GTA	ч	CIC
			വ	CCA	ø	GCT	4	GCA	×	AAG
archaeal		64)	ø	GCC	ø	GCA	×	AAG	н	ATT
		NO:	н	ATT	ø	CAA	×	AAA	Ω	GAC
le for	GI GI	Oi Oi	д	CCA	囟	GAG	ø	GCA	ы	GAA
gene	.3081) (SEQ	(SEQ	ч	TTA	လ	AGC	н	ATC	>	GIC
furiosus	No: AB013081) sequence (SEQ	ence	闰	GAA	>	GTT	ы	GAG	×	AAG
furi	No: sequ	sequence	Ö	GGA	æ	AGA	н	ATT	>	GTT
gno	ION	acid	Σ	ATG	ø	CAG	ø	GCT	E	ACC
Pyrococcus	(ACCESSION Nucleotide	Amino a	Σ	ATG	ø	GCT	×	AAA	×	AAG

Figure 17B

(HMf-like)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65) Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

18 54	36	54 162	69
GGT	E	R AGA	
A GCT	E GAG	GGT	
K AAG	L	A GCA	
r aga	CAC	H	
I	E	K	S
ATA		AAG	S
L	A GCA	A GCA	N F F
R AGA	$_{ m L}$	L	I TT
DGAC	v GTA	D GAT	A I
V	K	V	l
GTT	AAG	GTA	L
P	A	A	X
CCA	GCT	GCA	K
₽	A	K	D I
GCC	GCA	AAG	
I	CAA	K	ם
ATT		AAA	מ
PCCA	E	A	E
	GAG	GCA	E
L	S	I	ک ان
TTA	AGC	ATC	کا
E	V	E	K V
GAA	GTT	GAG	
g	r	I	باً <
GGA	Aga	ATT	
M	Q	A	Η
ATG	CAG	GCT	
M ATG	A GCT	к дад	N N D D

G G G //

V GTG r CTG CIC V GTC CGG ဗ ည AAG (CCC E GAG F TTT CTC GCC r CTG MATG S G AGT GGG P V T GTC ACT

ACC ACC ACC CIC စ ညီ K AAG r CTG gcc Gcc CAC F T ACC GGC CGC Y A GCC r CTG CAC CAC ဗ္ဗဗ္ဗ GAC

K AAG r CHC r CTC s AGC K AAG A GCC F ဗ ဗ္ဗ X TAC A V GCG GTC CAG V GTG P CCG GAG g GGG CGG S AGC

မှ ည A GCC AAG AAG gg G GAC $_{
m TTT}$ V GTC V GTG I ATC V GTG A GCG GAC ი მმ D GAC GAG AAG r CTC နှင့်

CCA TACG ကို ည A GCC R CGG ဝ ၁၅၅ A GCG K AAG X TAC ი მმმ ව පු Y TAC A GCC E GAG CAC rg CgC F s TCC g GGG CIG r Si DGAC V GTG L CTG E GAG K AAG I ATC r CTC ggc B r CTC o g R GGG CCC F TTT GAC GAG

L န္ A GCC L CTG V GTC DGAC GAC A GCG GAG Y TAC ggc P CCG V GTC E GAG CTC CGC P A GCG LCTG

A A GAC gg A T ACC CTC R I CGC ATC V GTC GAG Y ဗ္ဗဋ္ဌ E GAG A E K GCG GAA AAG K AAG A K GCC AAG

Y ය ශීශීශ E GAG CCC CAC V L GTC CTC D R I H GAC CGC ATC CAC s TCC CTT Q L CAG CTC (Y TAC D L GAC CTT

W TGG CAG CAG GAC ည် r Agg $_{
m L}$ ggc 0 X TAC A.A.G GAA W L A W GCC TGG P CCG T L I CTC ATC

K AAG V GTC ი წვვ CCC LCTT AAC z GAC 1 Д s TCC E GAG GAC Ω GGG ט T CTG A GCC CGG Y GAC A GCC

E r CTG S AGC TGG E GAG GAG r GTG CIT K AAG A R GCG AGG 1 T ACG K AAG GAG ი მმმ I ATC

r G I ATC K AAG GAG CGG I ATC gcc Gcc ည် K AAG CIG ცც D GAC CTG AAC AAG r L gcc Bcc

D GAC 4 CC မှု ညီ V GTG K AAG A GCC L CTG GAC ¥ s TCC CIC K AAG r G D GAT D GAC M M CAC g G G

ı İ R RGG E සු වූ DGAC r CCC E R CGG R AGG K AAA A G F GAC V GTG E r ကို ည CIG

먑 ဗ္ဗဋ္ဌ F TTC E GAG CAC CTC CIC s AGC g GGC F TTT E CIT R AGG GAG CIG FTTT A GCC R AGG

A ი მმ GAA CCG GCG က္ခ ₩ TGG P A GCC GAG GAG L gcc Bcc K AAG က ည s AGC E GAA r CTG

AGCC r CTG CTT D GAT A GCC \mathbf{W} M ATG CCC E K AAG R CGC န Tcc CII V GTG F TTT မှ ဗ GTG >

F

A AAA A Y TAT CCT E GAG CCC GCC GCC CGG CAC V GTC CGG ဗ ဗ္ဗ ი მმ R AGG gcc Gcc GCC A GCC L CTG

r G V GTT s AGC CTG GAC K AAA GCC CC CIC L ი გე R CGG A GCG E k AAG L GAC R AGG CIC

A GCC r CTC r CTC MATG မှ ည GAC D GAC ဗ္ဗဗ္ဗ က် သည် မှာ လူလူ CIC ဗ္ဗဋ္ဌ CTT ဗ္ဗဋ္ဌင E GAA R AGG r CTG A GCC

ဗ္ဗဋ္ဌ Y TAC မှ ည CGG A GCC v GTG ი ცვვ EGAG P CCC TACC T ACC N AAC s TCC CCT D GAC r CTG CTC Y

F r Si R AGG E GAG S TCC CIT A GCC gcc Bcc CGG E GAG ი ශීශීශී A GCG E GAG E GAG TACG ¥ FG E GAG ဗ ဗ္ဗ

R GGG Y CIT ¥ CT LCTC R AGG E E GAG ი მმ E CIT R AGG ය ශීශී ¥ TGG r G N AAC 30C

V GTG တ္မွ ACG A GCC E GAG M ATG H A GCC r CTG V GTC A B S CIT GCC R AGG E V GTG E

I ATC E GAG E A GCC V GTG E GAG r CTG S $_{
m TTG}$ A GCC r Agg CIC Y TAT A GCC V GTG D GAC LCTG ဗ္ဗဋ္ဌ

FIGURE 17B (CONT.)

A T ACC Y TAT I ATC AAC I ATC T ACG S AGT R AGG F I ATC A မှ ည r CTG CAG CAG DGAC M ATG T ACC A GCC EGAG r CTC R AGG ч Қ CTA F LCTG AAG N AAC CIG E က် R GG g gg N AAC W TGG E GAG CCC CCC CAC E A GCC FTTC ဗ္ဗဋ္ဌ r CTT A GCC S AGC V GTC R CAG CŢŢ V GTG I ATC P CCG D GAC GCC ကို ည g GGG A GCC Y T ACG A GCG s TCC F L L CTA TTG CAC CIA A GCC o CAG CIC A GCC T ACC g GGC T ACC GGG CTC Y S ဗ္ဗဋ္ဌ S AGC r CTG DGAC T ACG සි E GAG CGC යු දු E යු වූ gg A GAC ACC I ATC P CCG A GCC V GTC W CHC TACG M ATG САС EGAG ഠ s Tcc k AAG L TTG T ACG GGC CGC G GGG CAC CAC L gcc Gcc CTG F I ATT Н E I ATC E GAG A GCC GGC r CGC GGC CAG I CCC s TCG CHC IIC TIC LCTG E DGAC V GTC k AAG V GTG GAC N AAC N AAC GAC M ATG F A GCC V GTC I ATC I ATT F CAG CAG A GCC V GTG V GTG R AGG g GGC ය දු g GGC CAG F I TTC ATC L R CTC AGG Y ი მჭმ A GCC E GAG e Gaa T ACC CCC GGC CGC r Si Y TAC AGCC Н. A GCC K AAG ACC T ACC N AAC E GAG E GAG CTG CAC CIC EGAG 3 CAG E GAG S AGC E A GCC H မှ ငြင်င A GCC CAG ය වූ V GTC E GAG æ r CHO K AAG GAC E r CHC I ATA F က္ရွင္သ ACG DGAT ව වූල Y GGC Q CAG K AAG r CTG rg CGC န ၂၄၄ ය පු V GTC V GTC F GGG GGC CCT 3 3 3 3 5 5 r CTC K AAG ဗ္ဗဋ္ဌ S AGC ဗ္ဗဋ္ဌ N PAC S යි S AGC I ATC R GGG I ATC

V GTG CGG CTG GAG GAG GGC AGG AGG CGG V E T L F G R R Y V P D L E A GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC ATT GAG AAG ACC AAG GTG CGG GCC TGG

g GGC CAG V R E A A E R M A F N M P V GTG CGG GCG GCC CGC ATG GCC TTC AAC ATG CCC GTC K S AAG AGC C

EGAG r CTG T A A D L M K L A M V K L F P R ACC GCC GCC CTC ATG AAG CTG GCT ATG GTG AAG CTC AGG A GCC L L Q V H D E L V L E CTC CTT CAG GTC CAC GAG CTG GTC CTC GAG E M G A R M GAA ATG GGG GCC AGG ATG

ი მვვ E GAG V M GTC ATG A E A V A R L A K E GCG GAG GAG GAG GCG GTG GCC CGG CTG GCC AAG GAG r AGG E GAG P K CCA AAA

¥ TGG GAC V Y P L A V P L E V E V G I G E GTG TAT CCC CTG GTG GAG GTG GGG ATA GGG GAG

CAT H L S A K E G I D G R G G G H H CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT

H H * CAT CAT TAA

Figure 17C

Tag DNA polymerase- (HMf-like) fusion protein

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 64) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)

GGC GGC GGT

GTG V T S G M L P L F E P K G R V L L GTC ACT AGT GGG ATG CTC CTC TTT GAG CCC AAG GGC CGG GTC CTG

- T ဗ္ဗဋ္ဌ K AAG CTG A GCC CAC F T ACC ස වි Y A GCC r CTG
- X AAG r S r CIC s AGC AAG F A TTC GCC ပ္ပင္သ Y TAC v GTC A GCG CAG V GTG P CCG EGAG ය යිය R CGG s AGC
- P A SC C K AAG A GCC GAC $_{
 m TTT}$ v GTC V GTG I ATC V GTG A GCG D GAC ი მვ GAC GAG K AAG r CHO A 3CC
- CCA T ACG မှ ပြင် **G**CC ස දු ဗ ဗ္ဗ A GCG K AAG Y TAC ი მვვ g GGG Y TAC A GCC E H က္က င္ပင္ပဲ F S
- G G G r CIG CTC Б GAC V GTG $_{
 m L}^{
 m L}$ GAG K AAG IATC CIC A GCC r CTC GA & R ကို ည F I'I'I D 3AC E
- r CTG SAGC A GCC r Grg V GTC DGAC GAC A GCG GAG Y ဗ္ဗဋ္ဌ P CCG V GTC E r CTC rg CgC A GCG r CTG
- X A GAC gcc Gcc T ACC r CTC R I CGC ATC V GTC E Y ရ ၁၅ E K AAG E GAA A GCG K AAG K AAG A GCC
- Y IAC ව වූව E P CCC H CIC V GTC Н R I CGC ATC DGAC S TCC CŢŢ CTC o CAG Y TAC CTT GAC
- W cag Cag DGAC P CCC R AGG r CTG . 000 000 Y ·K AAG GAA W LCTT W TGG BCC. P CCG ₽ ACC IATC CTC
- K AAG V GTC g GGG P CCC CCC LCTT N AAC GAC 2 S GAG GAC ი მმმ ACC. r CTG A GCC CGG TAC × D GAC A GCC
- GAA $_{\rm CTG}$ s AGC ი მმც W TGG E E r CTG L K AAG R AGG A GCG T ACG K AAG EGAG ი მვვ IATC ဗ ဗ္ဗ
- r Eg I K AAG GAG R CGG I ATC A GCC က္ခ K AAG r CTG යියි GAC r CTG N AAC K AAG CHO r G 3 3 5 5 7
- GAC ACC. GGC SGC v GTG K AAG GCC GCC r CTG GAC W န TCC CTC K AAG CTG DGAT GAC M ATG CAC
- œ

A 3CC A GCC A r CTG A GCC ဗ္ဗဋ္ဌ ı E F V GTG IATC ۳. اظ AAC AAC V GTT L Y E ဗ္ဗဋ္ဌ G 3GG r CTG K AAA Y G GGG r CTC r CTC r CTT E GAG r TTC 3AA Y TAT S AGC r CTC CTT සි R AGG TACG N AAC GAC CGG GAG ы F D GAT PCCT E GAG P. CCG r CTG M ATG ය පි E W A GCC A GCC DGAC EGAG V GTG H A GCC E CTT P CCG CCC A GCC S TCC က္ခ g GGG L E CTG GAG (H M CAC ATG r CTC W TGG GCC CCC K AAA D GAC V GTG CAC AGG CGG GAG CCC P CCC CIT r CHC M ATG ဗ္ဗဗ္ဗ DGAC G GGG r CTC ₩ TGG A GCC A GCC A GCC R AGG s AGC CCC CTC E မှာ ය ලේශ g GGC A GCC S TCC DGAC A GCC EGAG A GCC ဗ္ဗဗ္ဗ E GAG H A GCC $_{
m CTT}$ CCC က ည සි දි EGAG r CTG $_{
m TTG}$ r CTG F TTT L R A CTC AGG GCC R K CGC AAG F E V GTC . GGG CCG E T ACC GGG V GTC යි දි TTC GCC AAA J CTC E GAG E GAG CIC F TTC (T ACC E GAG ය පි R CGG G GGG A GCT V GTC CTT r CTG S TCC N AAC L යියිය A GCG တ တို့ A GCG s TCC V GTC GAC Y TAT R AGG A GCC LCTT s TCC LCTT G GGG GAG CIT E R AGG E GAA A GCC E A GCC GAG GTG K AAG V GTG R AGG k AAG မ ဗ PCCT E G GGG က် ည LCTG GCC D GAC F A GCC $_{
m CTG}$ E GAA T ACG TGG R AGG V GTG E F TTT S AGC ი ცვე A GCC D GAC R AGG r CTG W L CTG E GAC L GAC GAA CIG CCC A S V GTG A GCC R AGG r CTG $_{
m L}^{
m L}$ E N AAC V GTG $_{
m L}$ rg CGC GGC (A GCC A GCC F Y 999 CTC E R AGG L L 3CC

A GCC R AGG Y TAT I ATC F IATC d b Y F CC F Q S AGT A GCC V GTG CAG CAG GAC CIA CIG M ATG ACC CTA F ი მვი r E R GG R G G CAG N AAC CIG E မှ ည R AGG ი მმ r CTG ¥ TGG K AAG E GAG S AGC A 225 V GTC සි දි d GTC ဗ ဗ္ဗ A GCC E ස ව් H r CTT S AGC 3 GCC CAG CAG R AGG E ပိုင္ပင္ပ A GCC Y T ACG ය වි V GTG GAC GCC I ATC අ පි s TCC F TTT R AGG r CTA M ATG R T CGC ACC ₽ GCC CAG r. CTC A GCC r Trg ဗီဗ္ဗင TACC ය රයය r CTC Y TAC ဗ္ဗဋ္ဌ D GAC N AAC s AGC S GAC T ACG L CTA E ဗ္ဗင္ဗ FTTC CIG R CGC မှ ည EGAG ය ද්ර ACC V GTC IATC ပို့ မှ A GCC ¥ TGG r Gid ACG M ATG H E E V GTG A GCC S ი მმმ H K AAG L TTG ACG P CCC CAC CIG ¥ TAC M ATG A GCC I ATT CIG E A GCC GGC SGC E GAG ကို ည CAG I ATC IATC က ည s TCG F အ ည GGC CGC ACC k AAG N AAC V GTG GAC N AAC E GAG r CTG GAC GAC E GAG M ATG A GCC K AAG ස වි ဗ ဗ္ဗ IATC I ATT CAG ₽ 000 v GTG . ദദ് F or CTG ဗ ညီ E GAG CAG မှ ၁ gg A ACC ကို ည ч Б I ATC R AGG Y ස වි ი გმ **4** 000 Y TAC A GCC ဗ ဗ္ဗ ₽ 9 9 9 I ATT K AAG CAC N AAC F r CTC E GAG F G ACC GAG CIC F E GAG W TGG E GAG 3 3 3 3 4 ကို ည ₽ 9 E CAG s AGC CAC R CGG V GTC E GAG 3 GC r CFC ස වි E DGAT ය වූ F AAG r G I ATA က ည် ი მვშ ACC V GTG Y සි පි ဗ္ဗဋ္ဌ 2G 25 CAG V GTC V GTC r G မှု ပိုင္ပ S s AGC F CCT V GTG E GAG ဗ ဗ္ဗ 크 AAG ပ္ပင္ပ S AGC IATC s AGC සු පු ဗ္ဗဋ္ဌ N AAC IATC AAG > P.

						18 54	36 108	54 162	6
E GAG	A GCC	9 999	W TGG	H CAT		g GGT	E GAA	R AGA	
L CTG	E GAG	EGAG	D GAC	H CAT		A GCT	E GAG	G GGT	
r Agg	CTC	M ATG	e Gag	H CAT		K AAG	L	GCA GCA	
CCC	V GTC	v GTC	ი მმმ	H CAT		r Aga	H	CA C	* TGA
F TTC	L CTG	e Gag	I ATA	ი მმმ		I ATA	EGAG	K AAG	s AGC
CTC	E GAG	k AAG	ე მ	g GGC		CIT	A GCA	A GCA	K AAG
K AAG	DGAC	A GCC	V GTG	G GGA		R AGA	L	L	I ATT
V GTG	H	L	EGAG	9		DGAC	V GTA	D GAT	A GCA
M ATG	V GTC	R CGG	V GTG	R CGC		V GTT	K AAG	V GTA	r CTC
A GCT	CAG	A GCC	EGAG	9 9		P CCA	A GCT	A GCA	K AAG
L	L	V GTG	L	D GAT		A GCC	GCA	K AAG	I ATT
K AAG	L	A GCC	P CCC	I ATT	•	I ATT	GA &	K AAA	D GAC
M ATG	M ATG	EGAG	V GTG	ი მმე		P CCA	E	A GCA	E GAA
L	R AGG	A GCG	₽	E		L TTA	s AGC	I ATC	V GTC
GAC	A CCC	R AGG	L	K AAG		e gaa	V GTT	e Gag	K AAG
GCC	ი მმმ	E GAG	A CCC	A GCC	>>	G GGA	r Aga	I ATT	V GTT
GCC CC	M ATG	K AAA	Y TAT	s TCC	H CAT	M ATG	CAG GAG	A GCT	T ACC
T ACC	E GAA	Ф ССА	V GTG	L CTC	H	M ATG	A GCT	K AAA	K AAG

Figure 17D

Pfu DNA Polymerase (WT) -(HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 61) //Nucleotide sequence (SEQ ID NO: 63)

ccetggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc totaacotgg gttatagtga caaatottco tocaccacog cocaagaagg ttatttotat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt cottocaatg gaaattcagc tttcaagatt agttggacaa cotttatggg atgtttcaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagotoca aacaagocaa gtgaagagga gtatcaaaga aggotcaggg agagotacao aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag tagagocota tatocotoga ttataattac coacaatgtt totocogata ototaaatot aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagettgeca attatgaaat tecaceagag aagetegeaa tatatgagea gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa aggogatggt ccaattagca atagggcaat totagotgag gaatacgato ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta ttttattctt tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ttccggggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgetteece aggaatgagg ttgttgtage tenteeenga aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac aagattgaga tgttcttgg //

54 108 162 GAG CAC CTT GAG GAA AAG CAC GCA GGT AGA GTT GAC AGA CTT ATA AGA AAG GCT GGT AAG GTA CTT GCA GAG CAC CTT GAG GAA GTA GAT CTT GCA AAG CAC GCA GGT AGA CTC GCA ATT AAG AGC TGA ATG ATG GGA GAA TTA CCA ATT GCC CCA GCT CAG AGA GTT AGC GAG CAA GCA GCT AAA GCT ATT GAG ATC GCA AAA AAG GCA AAG ACC GTT AAG GTC GAA GAC ATT AAG

Figure 17E

(HMf-like) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 61)

54	108	162	
GGT	GAA	AGA	
GCT	GAG	ggT	
AAG	CTT	GCA	
AGA	CAC	CAC	
ATA	GAG	AAG	AGC
CTT	GCA	GCA	AAG
AGA	CIT	CIT	ATT
GAC	GTA	GAT	GCA
GTT	AAG	GTA	CTC
CCA	GCT	GCA	AAG
ggg	GCA	AAG	ATT
ATT	CAA	AAA	GAC
CCA	GAG	GCA	GAA
TTA	AGC	ATC	GTC
GAA	GTT	GAG	AAG
GGA	AGA	ATT	GTT
ATG	CAG	GCT	ACC
ATG	GCT	AAA	AAG

		_	_				_			_	_	_
gtcgc	ctat	agaac	gtgge	aaatt	gatto	attgt	sttta	gcagt	ggcct	ctcta	зааа	caac
atgaagaatc ccccagtcgc	ttatttctat	tatagagaag	ataatgattt tagatgtgga	acggaaaatt	taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc	tgagaattgt	ggaaacttta	atccagcagt	acaaaggcct	aaaccctcta	cagatgaaaa	ttgtatcaag
atc c			itt t		ica g							
aagaa	cccaagaagg	taagtatagt	atgat	aaaaaagaga	atta	ggaaagattg	attaccgtgt	gttagagaac	tacctcatcg	ttcgatatag	attagttatg	gttga
atg					gata							tace
cttt	accg	ttt	Igagc	attc	ttac	Igcat	gaat	aaaa	gaga	tgcc	aatg	tcca
atatgttctt actcgccttt	caaatcttcc tccaccaccg	cctcccctat tttctctctt atgagatttt	gttttatact ccaaactgag ttagtagata tgtggggagc	aacctgttat taggctattc	acat	aaataacggg ggaaaggcat	aaaagtttct cggcaagcct	tagagaaaaa	tgcaaagaga	gattcttgcc	aattataatg	agatcttcca tacgttgagg
r ac	n ţ	r a	ه بر	n ţţ	n at	99	η Ω,	n Ç				
ttati	ctta	ctcti	agati	gtta	agacı	acgg	ttta	acta	ccati	ctaa	ggcc	aaca(
tatg	aaat	ttct	tagt	acct	ttt	aata	aaag	ttcccactat	atattccatt	aagagctaaa	gaaaaggccc	ggaaaaacat
		t t	g t	ರ ರ	ro ro							
caca	agtg	ccta	ctga	agga	taga	taag	tgag	agat	atac	ggaa	gtt	tact
gggtccacat	gttatagtga	gtaa	:aaa	gaagaaggaa	atga	gaagttaaga	aaggttgaga	ccccaagatg	ttcgaatacg	gaggggaag	gaagagtttg	gtgattactt
		ŏ	ŏ		ບ							
ccctggtcct	tctaacctgg	caactctaca	tact	ttacataact	agag	aaagattgaa	tgatgtagag	tttggaacat	tgtggacatc	aataccaatg	tcacgaagga	tgaagcaaag
tgg	aac	icto	tta	ıcatı	ıgat,	igat	ıtgt,	gga	gga	acc	ıcga	lagcs
CCC	tct	Caê	gtt	tta	taa	aaa	tga	ttt	tgt	aat	ta	tga

ttocgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg tegtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag aggegatggt ccaattagca atagggcaat tctagetgag gaatacgate ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagata gatgctacct aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt cottccaatg gaaattcagc tttcaagatt agttggacaa cotttatggg atgtttcaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaaatactc cttgactata gacaaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta gaaggagote gaagaaaagt ttggatttaa agteetetae attgaeaetg atggteteta tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag tagagocota tatocotoga ttataattac coacaatgtt totocogata ototaaatot ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg gggattette gttaegaaga agaggtatge agtaatagat gaagaaggaa aagteattae

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgetteece aggaatgagg ttgttgtage tenteeenga TGA aagattgaga tgttcttgg //

Figure 17F

(HMf-like) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 27) Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 28) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 GAG GAA GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA CTT ATA AGA AAG GCT CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC // TTA AAA GCT ATT GAG ATC GCT CAG AGA GTT AGC GAA ATG ATG GGA

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT TCTTGCCTTC AAAAGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG CCACTATTAG AGAAAAGTT AAAGAGATAC TCTTCCATAC TATCAGGGAG ATATTTAGCG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TTCCATTTGC AAAACATAGA TTCTCAGGAT TACTIATAAT GGAGACTCAT TCGCATTCCC AGCAAAGGTG ATTACTTGGA GGACATCTTC GAATACGATA CAAGATXXXC GAGAGATG ATAAAGAGAT GGAACATCCC GAATTGTTGA AACTTTATTT CAGCAGTTGT AAGGCCTAAT ACATTATAGT CCCTCTATCA ATGAAAATGA TATCAAGCGA ACCGTGTGGA GATATAGAAA AGTTATGCAG AAGATTGTGA AGAGAACATC CTCATCGACA AAGGATCCTG GTTGAGGTTG

1620 1320 1440 1500 1560 1680 1740 1800 1020 1140 1200 1260 1380 1860 1920 1980 2040 2100 2160 2220 1080 TTTCGACTTG TGGACAACCT ACTTAGGAAA TCAAAGAAGG AAAGAAAAG TGTATATGAA AGTAGGCCAC GTTAGAGGAA GCTTGAATAT GGCAACTTAT GTGGGAAAAC TTATGGCTAT GGGAAGAAAG CCTCTACATT TGAAGAAGCT ACCAGAGAAG AGGTCCTCAC AGCTGAGGAA AGCCTGGGAA CAATGITICI AATACTCCTT TGAAATTGCA AATGGTAATT GGTTCTTCCA AATAGATGAA ATACCAAAAG GAAGTCAAGG GAAGAATACA AGTGGTTCTT AGATAGCAAA CAAGATTAGT AAGAGGAGTA CACTAGAGGC AAGATGCAAA AAAAGGGGTT TAATTACCCA TCGCTCCTCA TGGGACATTT CTATAGAAAA TCTACGGATA TTACTGCCTG GATTTAAAGT GTGAGGAAAT GACTGCTAGA GGTATGCAGT GAGATTGGAG ACGGAGATGT ATAAGGCGAT CGATGGTCCA ATTAGCAATA GGGCAATTCT GGGATTTGGA TACAGAAAGG AAGACCTCAG ATGAAATTCC TAAAGCCAGG TGGAGAACCA TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // TACTCGATGG AACCTTGTAG AAGCCAAGTG GCTGAGAGCG GGAGGAGAAA TGGTTTAGAG ATAGTTAGGA ATACTAAAAC TTACATGAGT CCAACATACA TACGCCGACG AAAGAGCCAG AACTATGATA GCAAATTCTT GAAAAGTTTG CTTGCCAATT ATTCAGCTTT CCCTCGATTA ACTCAAGATC AAGCTCCCTG AGCTGCTAAA GGAGTTAAAA GAATATTACA CCAAGTCTCT ACGAAGAAGA AAGCACAGGG GGGATGCAAG TTTGGAGACA TAGGCGATAT GACGGCTGTA AGTTGCCAAA TCCAATGGAA AGCTCCAAAC TGGTTTTATA AATGAAGGAA TAAGGAGTGT GGAGCTCGAA AACAAGACCA TGGATTCGTT AGCCCTATAT AAAACTCTTA AACTATCCCA CATAAATTCA ATTCTTCGTT GTATGACGCA AATAAATCTC GGAGAAGGTA AATACAAAAG ATGAGCAGAT TAACAAGGAC TTTCAAGGTC TAGTATGGAA ACCTTGAGAG TAGATTTTAG TTAAGACAAA AAAAAGCGAT GATGGTACTG GTCTCTATGC AAGCTAGAGT CAAAGAAACT GAAAGCCAAA AAGAATTCCT GAAACGAAGT GCTACACAGG TAAATCTTGA AGGACATCCC ATAAGAGGG TAAAAGAAGT TTGTAAAATA TCATTACTCG TACTTAGAGG AAAAGCACAA GGATATTGGA ATGCAGAGAA AGTGGAGAGA GACTATAGAC **TATCATGTAA** GAACTCGGGA ATAGTATACC GCAAAAGCAA CTCGCAATAT TACGATCCCA GCGGTACTTA ACAAGACAAG GCAATTTTG TTATGGGATG CCCGATACTC AAGTTCTGCA AGACAAAAGA GACACTGATG GCTCTAGAAT GAAGGGTTTT GCCTACGAAA CTCAGGGAGA TACATCGAGT GAAGGAAAAG AAAGAAACTC GTGAGAATAG GTAGCTGTTG GGATACATAG

Figure 17G

PFU DNA POLYMERASE (V93 R OR E)-(HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 63)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1080 1140 1200 1260 1320 1380 1500 1560 1620 1680 1740 1800 1860 1920 2100 2040 1020 1440 1980 960 480 540 900 999 780 840 900 GITAAGAAAA TAACGGGGGA AAGGCATGGA CAAGCCTATT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG TTAGACCATA CATTTACGCT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT IACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA CTGTTATTAG GCTATTCAAA AGAAAAGTT TATAATGATT TCTTCCATAC TATCAGGGAG TTTCGACTTG TGTATATGAA AGCCTGGGAA GGCAACTTAT TGGACAACCT ACTTAGGAAA TCAAAGAAGG GTGGGAAAAC CAATGTTTCT AGTAGGCCAC GTTAGAGGAA TTATGGCTAT AAAGAAAAG GCTTGAATAT AATAGATGAA AGGTCCTCAC AAAGAGATAC TCTTGCCTTC ATATTTAGCG CGAGCCCAAG AATACTCCTT GGGAAGAAAG CCTCTACATT TGAAATTGCA AATGGTAATT AGCTGAGGAA V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) AGCAAAGGTG ATTACTTGGA AAAACATAGA AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA AAGATIGIGA GAATIGITGA IGTAGAGAAG GTIGAGAAAA AGITICICGG CCACTATTAG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TTCTCAGGAT GAGATGGAAG CCAACATACA CACTAGAGGC TACGCCGACG AGATAGCAAA TCCAATGGAA ATTCAGCTTT CAAGATTAGT AAGCACAGGG AACCITGIAG AGIGGIICIT GGGATGCAAG AACTATGATA TCGCTCCTCA TGGTTTTATA CCAAGTCTCT TGGGACATTT CTATAGAAAA TCTACGGATA GTGAGGAAAT GAGATTGGAG TAAAGCCAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT TTCCATTTGC TCGCATTCCC GAAGAATACA AAGATGCAAA TGGATTCGTT AAAGAGCCAG AAAAGGGGTT TAATTACCCA TTACTGCCTG GGAGCTCGAA GAAAAGTTTG GATTTAAAGT GACTGCTAGA GGTATGCAGT ATAAGGCGAT AGTIGCCAAA TACTCGAIGG ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC GAATACGATA ATAAAGAGAT GGAGACTCAT GAAGTCAAGG GCTGAGAGCG GGAGGAGAAA V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CAAGATXXXC ACCATTGGAA CCCTCGATTA CATAAATTCA AAGCTCCCTG ACGAAGAAGA TTACATGAGT GGAGTTAAAA GATAGAACTT AATGAAGGAA ACTCAAGATC GCAAATTCTT ATAGTTAGGA AAAGAGAACG GAAAATTTAA GATAGAGCAT CTTCTCAGGG ATGATTCAAA GATTGAAGAA GATTAAATTA GAGAGAGATG GGAGAAGGTA GGAACATCCC TACTTATAAT GACGGCTGTA AGCCCTATAT AAAACTCTTA TAAGGAGTGT AACTATCCCA AGCTGCTAAA AATAAATCTC ATTCTTCGTT AACAAGACCA GGACATCTTC TGGTTTAGAG AAGAATTCCT AAGGCCTAAT AACTTTATT TAACAAGGAC ACCTTGAGAG TTTCAAGGTC CAGCAGTTGT GAAACGAAGT TAGATTTTAG AGGACATCCC TTAAGACAAA GATGGTACTG AAGCTAGAGT TAAAAGAAGT CCCTCTATCA ATGAAAATGA TATCAAGCGA AAAAACTTGG TAGGCGATAT GAAAGCCAAA GCTACACAGG TAAATCTTGA AAAAAGCGAT TAGTATGGAA GTCTCTATGC TTGTAAAATA ATAAGAGGG TCATTACTCG ATGAGCAGAT CAAAGAAACT SGATACATAG TACTTAGAGG ACATTATAGT AAAGAAACTC GAACTCGGGA GAAGGAAAAG GTAGCTGTTG ACCGTGTGGA AGAGAACATC ATGCAGAGAA AGTGGAGAGA GCCTACGAAA CTCAGGGAGA ATAGTATACC GACTATAGAC GACACTGATG GTGAGAATAG CTCATCGACA GATATAGAAA AGTTATGCAG STIGAGGIIG AAGGATCCTG AAAAGGGCAG TATCATGTAA GCAATTTTG TTATGGGATG CCCGATACTC AAGTTCTGCA AGACAAAAGA GCAAAAGCAA TACATCGAGT GCTCTAGAAT GAAGGGTTTT CTCGCAATAT

108 162 GAA GCA AAG CAC GCA GGT AGA GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 GAG CLI AAG ATA AGA GAG CAC AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA GCA CHT ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // AGA AAG GTA CTT GCA AAA AAG GCA GTA GAT CTT GAC GTT CCA GAG CAA GCA GCT gcc ATT CCA AGC TTA GAG ATC GTT CAG AGA GCT ATT ATG AAA (GCT

Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR B) - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) or I) G387P Mutant (CCN is the codon for Proline where N = C, G, A, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

1140 999 840 540 CATTTACGCT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC AAGGCCCAAT TATAATGATT TTTCGACTTG TGTATATGAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA AAGGCATGGA CAAGCCTATT AGAAAAAGTT AAAGAGATAC TCTTCCATAC TATCAGGGAG ATATTTAGCG CGAGCCCAAG AGCCTGGGAA GGCAACTTAT TGGACAACCT ACTTAGGAAA GTTAAGAAA TAACGGGGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CCACTATTAG TTCCATTTGC AGCAAAGGTG ATTACTTGGA AAAACATAGA TTCTCAGGAT GAGATGGAAG CACTAGAGGC AGATAGCAAA CAAGATTAGT TITCAAGGIC AAGCACAGGG AACCIIGIAG AGIGGIICII TTAGACCATA TCGCATTCCC GAAGAATACA AAGATGCAAA CCAACATACA TACTCGATGG GATAGAGCAT GATAGAACTT CAAGATXXXC GAATACGATA GAGTTTGGAA GAGAGATG ATAAAGAGAT GGAGACTCAT ACCATTGGAA TACGCCGACG GAAGTCAAGG TCCAATGGAA ATTCAGCTTT GATTGAAGAA GGAACATCCC GGACATCTTC CGAAGGAGAA TACTTATAAT GATTAAATTA GGAGAAGGTA AGTTGCCAAA GACGGCTGTA AATAAATCTC GAATTGTTGA AAGAATTCCT GAAAATTTAA ATGATTCAAA AACTTTATTT CAGCAGTTGT AAGGCCTAAT ATGAAAATGA TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT TAACAAGGAC GAAAGCCAAA ACCTTGAGAG CCCTCTATCA AAAGAGAACG CTCATCGACA AGTTATGCAG CTTCTCAGGG AAGATTGTGA ACCGTGTGGA AGAGAACATC GTTGAGGTTG AAAAGGGCAG TATCATGTAA GCAATTTTTG AGTGGAGAGA GAACTCGGGA TTATGGGATG SCCTACGAAA GATATAGAAA AAGGATCCTG ATGCAGAGAA

1200	1260	1320	1380	1440	1500	1560	1620	1680	1740	1800	1860	1920	1980	2040	2100	2160	2220	2280	2328
GTGGGAAAAC	CAATGTTTCT	TCGCTCCTCA AGTAGGCCAC	GTTAGAGGAA	CTATAGAAA AATACTCCTT	TCTACGGATA TTATGGCTAT	GGGAAGAAAG	CCTCTACATT	GTGAGGAAAT AAAGAAAAG	GCTTGAATAT	AATAGATGAA	TGAAATTGCA	TGAAGAAGCT	ATGAAATTCC ACCAGAGAAG	AGGTCCTCAC	AATGGTAATT	AGCTGAGGAA	GGTTCTTCCA	ATACCAAAAG	
GCTACACACC MGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC	TAATTACCCA	TCGCTCCTCA	TGGGACATTT		TCTACGGATA	TTACTGCCTG	GATTTAAAGT	GTGAGGAAAT	TIGIAAAAIA CAIAAAIICA AAGCICCCIG GACIGCIAGA GCIIGAAIAI	ATAAGAGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA	TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA	TTTGGAGACA ATACTAAAAC ACGGAGATGT		ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC	CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT	TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA	AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA	AAGACCTCAG ATACCAAAAG	AATCC //
AAAGAGCCAG	CCCTCGATTA	AACTATGATA	CCAAGTCTCT	ACTCAAGATC	GCAAATTCTT	GCTGAGAGCG	TAGTATGGAA GGAGCTCGAA GAAAAGTTTG	GTCTCTATGC AACTATCCCA GGAGGAGAA	AAGCTCCCTG	ACGAAGAAGA	ATAGTTAGGA	ATACTAAAAC	AATACAAAAG CTTGCCAATT	TTACATGAGT	GGAGTTAAAA	ATTAGCAATA	GAATATTACA	GGATATTGGA GGGATTTGGA TACAGAAAGG	TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
MGGATTCGTT	TAGATTTTAG AGCCCTATAT	TAAATCTTGA GGGATGCAAG AACTATGATA	TGGTTTTATA	AATGAAGGAA	AAAAAGCGAT AAAACTCTTA GCAAATTCTT	TAAGGAGTGT	GGAGCTCGAA	AACTATCCCA	CATAAATTCA	ATTCTTCGTT	TGGTTTAGAG			AACAAGACCA	AGCTGCTAAA	CGATGGTCCA	GTATGACGCA	GGGATTTGGA	TTCCTGGCTT
GCTACACACC	TAGATTTTAG	TAAATCTTGA	AGGACATCCC	AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC		GATGGTACTG	TAGTATGGAA	GTCTCTATGC		ATAAGAGGGG	TCATTACTCG	AAGCTAGAGT	TAAAAGAAGT		CAAAGAAACT	TACTTAGAGG			TCGGCCTAAC
CTCAGGGAGA	ATAGTATACC	CCCGATACTC	AAGTTCTGCA	AGACAAAAGA	GACTATAGAC	GCAAAAGCAA	TACATCGAGT	GACACTGATG	GCTCTAGAAT	GAAGGGTTTT	GAAGGAAAAG	AAAGAAACTC	GTGAGAATAG	CTCGCAATAT	GTAGCTGTTG	GGATACATAG	TACGATCCCA	GCGGTACTTA	ACAAGACAAG

54 108 162 ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GCT CAG AGA GTT AGC GAG CAA GCT AAG GTA CTT GCA AAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA AAG ACC GTT AAG GTC GAA ATT AAG TCG TTA AAG GTC GAA ATT AAG AGC TGA

Figure 171

(HMf-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30) G387P Mutant (CCN is the codon for Proline where N=C, G, A, or T) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT

54

52/186

GCA GAG CAC CTT GAG GAA GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA GAA GAC ATT AAG CTC GCA ATT AAG AGC // AAG GTA CTT CAA GCA GCT GAG AAG ACC GTT AAG GTC CAG AGA GTT AGC AAA GCT ATT GAG ATC GCT

108

1440 1020 1080 1140 1200 1260 1320 1380 1500 1560 1620 1680 1740 1800 1860 1920 //ATGATITIAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 2100 540 840 960 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 TTCCATTTGC AAAGAGATAC AATAGATGAA CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA CAAGCCTATT AGAAAAAGTT TCTTGCCTTC TATAATGATT TATCAGGGAG ATATTAGCG CGAGCCCAAG TTTCGACTTG TGTATATGAA AGCCTGGGAA GGCAACTTAT TGGACAACCT ACTTAGGAAA TCAAAGAAGG GTGGGAAAAC CAATGTTTCT TCGCTCCTCA AGTAGGCCAC GTTAGAGGAA TTATGGCTAT GGGAAGAAAG AAAGAAAAG GCTTGAATAT ACCAGAGAAG AGGTCCTCAC AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT IACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA TCTTCCATAC AATACTCCTT CCTCTACATT TGAAATTGCA TGAAGAAGCT GTTGAGAAAA AGTTTCTCGG CCACTATTAG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT GAGTTTGGAA AAGGCCCAAT TTCTCAGGAT TCGCATTCCC GAGATGGAAG GAAGAATACA AGATAGCAAA AAGATGCAAA CAAGATTAGT AGTGGTTCTT TAATTACCCA TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TTTGGAGACA ATACTAAAAC ACGGAGATGT ATGAAATTCC CACTAGAGGC AAGAGGAGTA NGGATTCGTT AAAGAGCCAG AAAAGGGGTT TGGGACATTT CTATAGAAAA GCAAATTCTT TCTACGGATA GTGAGGAAAT GACTGCTAGA ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AAAACATAGA TTACTGCCTG GATTTAAAGT ATAAGGCGAT GGACATCTTC GAATACGATA GGAACATCCC CAAGATXXXC ATTACTTGGA ATAAAGAGAT ACCATTGGAA TACGCCGACG TACTCGATGG AAGCACAGGG AACCTTGTAG AAGCCAAGTG CCCTCGATTA AACTATGATA ACTCAAGATC GCTGAGAGCG GGAGGAGAAA CTTGCCAATT GGAGACTCAT GAAGTCAAGG CCAACATACA TCCAATGGAA ATTCAGCTTT CCAAGTCTCT GAAAAGTTTG AAGCTCCCTG TTACATGAGT TGTAGAGAAG CGAAGGAGAA AGCAAAGGTG GAGAGAGATG TACTTATAAT GGAGAAGGTA AGTTGCCAAA AGCTCCAAAC AGCCCTATAT GGGATGCAAG GATTAAATTA GACGGCTGTA TGGTTTTATA AAAACTCTTA AATACAAAAG AATAAATCTC AATGAAGGAA TAAGGAGTGT GGAGCTCGAA AACTATCCCA CATAAATTCA AACAAGACCA GAATTGTTGA AACTTTATTT CAGCAGTTGT AAGGCCTAAT CCCTCTATCA AAAAACTTGG ACCTTGAGAG TTTCAAGGTC GCTACACACC TAAAAGAAGT ATGAGCAGAT CAAAGAAACT TACTTAGAGG ATGAAAATGA TATCAAGCGA ACATTATAGT TAGGCGATAT TAACAAGGAC GAAAGCCAAA AAGAATTCCT GAAACGAAGT TAGATTTTAG TAAATCTTGA AGGACATCCC TTAAGACAAA AAAAGCGAT GATGGTACTG TAGTATGGAA GTCTCTATGC TTGTAAAATA ATAAGAGGG TCATTACTCG AAGCTAGAGT CTTCTCAGGG CTCATCGACA AAGGATCCTG CTCAGGGAGA GACTATAGAC GCTCTAGAAT GAAGGGTTTT AAGATTGTGA ACCGTGTGGA AGAGAACATC GATATAGAAA AGTTATGCAG GTTGAGGTTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCAATTTTTG AGTGGAGAGA GAACTCGGGA TTATGGGATG GCCTACGAAA ATAGTATACC CCCGATACTC AAGTTCTGCA AGACAAAAGA GCAAAAGCAA **PACATCGAGT** GACACTGATG GAAGGAAAAG AAAGAAACTC GTGAGAATAG CTCGCAATAT GTAGCTGTTG GGATACATAG

GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG

Figure 17J

(HMF-LIKE) - PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GAG GAA GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAA GAC ATT AAG CTC GCA ATT AAG AGC // GAG ATC ATG GGA GAA TTA CAG AGA GTT AGC ATG ATG GGA GCT ATT AAG ACC AAA GCT

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 600 840 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 999 AAAGAGATAC ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC TATAATGATT TCGCATTCCC ATAITIAGCG CGAGCCCAAG TTTCGACTTG GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA TGGACAACCT CAAGCCTATT AACTITATIT GGAACATCCC CAAGAIXXXC CCACTATTAG AGAAAAGTI TCTTCCATAC GAGAGAGATG ATAAAGAGAT TTCTCAGGGAT TATCAGGGAG TGTATATGAA GGCAACTTAT TTCCATTTGC GTTGAGAAA AGTTTCTCGG GAGTITGGAA AAGGCCCAAI GAGATGGAAG CACTAGAGGC ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA CAAGATTAGT AAAACATAGA GAAGAATACA GGAGACTCAT GGACATCTTC GAATACGATA ATTACTTGGA GATTAAATTA ACCATTGGAA TCCAATGGAA ATTCAGCTTT GAAGTCAAGG CCAACATACA TGTAGAGAAG CGAAGGAGAA TACTTATAAT GACGGCTGTA AATAAATCTC AGCAAAGGTG ATGATTCAAA GAATTGTTGA CAGCAGTIGT AAGGCCTAAT CCCTCTATCA TATCAAGCGA ACATTATAGT TAACAAGGAC GAAAGCCAAA BAACTCGGGA AAGAATTCCT ATGAAAATGA AAAAACTTGG TAGGCGATAT AAGGATCCTG CTTCTCAGGG AAGATTGTGA ACCGTGTGGA CTCATCGACA TATCATGTAA AGTGGAGAGA GCNATAGCNA AGTTATGCAG GTTGAGGTTG AAAAGGGCAG ATGCAGAGAA AGAGAACATC SCAATTTTG

GCTACACA GGT_GGATTCGTT AAAGAGCCAG AAAAGGGGGTT GTGGGAAAAC 1200 1740 TITCAAGGIC AAGCACAGGG AACCTIGIAG AGIGGIICII ACIIAGGAAA 1080 GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 TAGATITIAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTITCT 1260 1440 1500 1680 1800 1860 1920 1980 2040 2100 2160 2220 2280 1560 1620 AGTAGGCCAC GTTAGAGGAA AATACTCCTT GGGAAGAAAG CCTCTACATT TTATGGCTAT AAAGAAAAAG GCTTGAATAT AATAGATGAA ACCAGAGAAG TGAAATTGCA TGAAGAAGCT AATGGTAATT AGCTGAGGAA GGTTCTTCCA TACAGAAAGG AAGACCTCAG ATACCAAAAG AGGTCCTCAC GGGATGCAAG AACTATGATA TCGCTCCTCA CTATAGAAAA GAATATTACA TGGAGAACCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT TCTACGGATA TTACTGCCTG GGAGCTCGAA GAAAAGTTTG GATTTAAAGT GGAGGAGAAA GTGAGGAAAT GGTATGCAGT GAGATTGGAG ATACTAAAAC ACGGAGATGT ATGAAATTCC ATAAGGCGAT CGATGGTCCA ATTAGCAATA GGGCAATTCT GACTGCTAGA TAAAGCCAGG TICCIGGCII AACAIIAAAA AAICC // TAAGGAGTGT GCTGAGAGCG TTAAGACAAA AATGAAGGAA ACTCAAGATC AAGCTCCCTG TTACATGAGT ACGAAGAAGA TGGTTTAGAG ATAGTTAGGA CTTGCCAATT GGAGTTAAAA GCAAATTCTT TTTGGAGACA AAAACTCTTA CATAAATTCA ATTCTTCGTT AACTATCCCA GTATGACGCA GGGATTTGGA AACAAGACCA AATACAAAAG AGCTGCTAAA TCGGCCTAAC AAAAAGCGAT GATGGTACTG TAGTATGGAA GTCTCTATGC ATAAGAGGGG AAGCTAGAGT ATGAGCAGAT TAAATCTTGA TTGTAAAATA TCATTACTCG TAAAAGAAGT CAAAGAAACT TACTTAGAGG AAAAGCACAA GGATATTGGA TTATGGGATG TACGATCCCA GCCTACGAAA CTCGCAATAT ACAAGACAAG CTCAGGGAGA ATAGTATACC AAGTTCTGCA AGACAAAAGA GACACTGATG GCTCTAGAAT STGAGAATAG GTAGCTGTTG GGATACATAG SCGGTACTTA CCCGATACTC GACTATAGAC GCAAAAGCAA TACATCGAGT GAAGGGTTTT GAAGGAAAAG AAAGAAACTC

TGA

Figure 17K

(HMF-LIKE) fusion protein PFU DNA POLYMERASE (D141A/E143A/V93R OR E)

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA CATTTACGCT TTAGACCATA GATAGAGCAT GATAGAACTT AAAGAGAACG GAAAATTTAA ATGATTCAAA CTTCTCAGGG AAGATTGTGA

ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300

AGAGAACATC	CAGCAGTTGT	GGACATCTTC	GAATACGATA	TTCCATTTGC	AAAGAGATAC	360
CTCATCGACA	AAGGCCTAAT	ACCAATGGAG	GGGGAAGAAG	AGCTAAAGAT	TCTTGCCTTC	420
GCNATAGCNA	CCCTCTATCA	CGAAGGAGAA	GAGTTTGGAA	AAGGCCCAAT	TATAATGATT	480
AGTTATGCAG	ATGAAAATGA	AGCAAAGGTG	ATTACTTGGA	AAAACATAGA	TCTTCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	009
AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTTAGCG	099
AAAAGGGCAG	AAAAACTTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
TATCATGTAA	TAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTATATGAA	840
GCAATTTTTG	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	006
AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	096
GAACTCGGGA	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTGTAG	AGTGGTTCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAGT	AGCTCCAAAC	AAGCCAAGTG	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACA GC	GGTGGATTCGTT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAC	1200
ATAGTATACC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCGATACTC	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTATA	CCAAGICICI	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAAGCGAT	AAAACTCTTA	GCAAATTCTT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCTG	GGGAAGAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACTATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAG	1680
GCTCTAGAAT	TTGTAAAATA	CATAAATTCA	AAGCTCCCTG	GACTGCTAGA	GCTTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
GTAGCTGTTG	CAAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTCCTGGCTT	AACATTAAAA	AATCC //		2328

54 108 162 A CTT ATA AGA AAG GCT GGT I GCA GAG CAC CTT GAG GAA I GCA AAG CAC GCA GGT AGA I AAG AGC TGA CCA ATT GCC CCA GTT GAC AGA GAG CAA GCA GCT AAG GTA GTA GAT CTT GCA AAA AAG GCA GTA GAT CTT GAA GAC ATT AAG CTC GCA ATT A ATG ATG GGA GAA TTA C
GCT CAG AGA GTT AGC G
AAA GCT ATT GAG ATC G
AAG ACC GTT AAG GTC G

Figure 17L

KOD DNA POLYMERASE - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 63) CGT (ALL POSSIBLE CODONS FOR ARGININE) 1140 1260 1380 1440 1500 1320 1020 1200 1080 999 840 900 960 CTGTCATAAG AATTTTCAAG AGAGGAGAGG TIGAACCCIA CIICIACGCC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG GGACAAGATA CCTTATGATA CGGCCAGTCC CCTCAGGAAG CGTCTCGCCG CGGCCACCGC GCTCCTCGAT AAGGGAGTAC CAAGCGCTAC GCTCGCCTTC CGAGCCGAAG CGTTTATGAA AGCCTGGGAA GGTCACATAC GGCCAGAAGA CGGCTATGCA CTACAGCGAC AAAGAAGGCT GAGACCAGTT TCTCCCCTAC TGTGAAGGAG CTATCTGAAA CTTCGATCTC GGAGAACATA GLUTAMIC ACID) TITITGCCAC AATACCIGGA GCCGAIGCIG AAACCGICAA CGGCCTGGGG CAGCGATAAG TACCCTTCGC AGCTGAAAAT AGAACGTGGA TCGACTTCGC GACGGATACA AAATAACCAC AGTCGCCCGC TACTCGATGG AAGATGCGAA CTCGCTTAAT AAAAGGAGCT TCGAGAGGAA AGTTCCTCGG TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT TCCTCCGTGT GGGATGGAAG CGCTTGAGGC CAGCACTGGC AACCTCGTTG AGTGGTTCCT GAGGGTTGTG TCACCCACAA CCCCACAGGT GAGACCTCCT ACGGTTACTA GATAGAGGAA AAGTACGGCT TTAAGGTAAT AATAAACTTC GCCCTCGGAA TACGCTGAGG AAGCCCGATG AGCCTGCTTG AACAGCTACT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT GTTCAGAAGA TGACATCTAC GAGTACGACA GGCGACGAGG ATAACTTGGA GGCGACAACT GAAGTGAAGG CCCACATACA TCCGATGGAG GCCCAGCTTT TCAATCATCA TATGACGTTG ATTGACCCGA V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CAGGACXXXC ATAAAGCGCT GAGCCCGAGA GGAGTGTGCA GAGAGCGTAA GGCCAGGGTG AACCTACAAC GAAGGCCACG ATGCAAGGAA ATTTATCCCG GGTTGAAAAG GAGGGAGATG GGCCCCGAAC CCTGTACCCC GATCCTGGCA TACTCATCCG GCCAATGGAA GATAAACCTG GGAGAAGGTT CTATGTAAAA GTTTGCCGTC CAGCAGTTAT AAAAGCTCGG ACAGAGAAGG ACTTCCCAGG AACTCTACTT CTCTCTACCA ACCTTGAGAG ATTTAGATC CCATCAAGGA ACGALTCTGC CGGTTAAGCG AGGGATTAGT ACGAGGAAGG TCTCGACGGA ACGITCICAL TGGGCGACAG TAAGACGGAC GTCAGCCGAA AGGAGTTCCT TCTCCCGCTC GGAATGAGCT ATGAAGGAGG AGAAGAAGAT GGGCCATCAA GGTACTGCAA ACCGACGGAT CTCCTGAAGG CTCTGGGACG GTGTACCTAG GATACGCTCA TTCTGCAAGG CAGAAGATAA AGGCGCGCT ACGGTTGTAA GAGGTCTGGA AGCTACGCCG ACCGGCGAGA GAGCTTGGGA GCCTATGAGA CGGCAGAGCT CGAGAGCATC CTCATAGACA GACATTGAAA GTTGACGTCG AAAGACCCGG AAGCGCTGTG ATTCAGAGGA TATCCTGTGA SCCGTCTTCG TACAGGCAGA ATAACGATGA

GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325	54 108 162	GGT GAA AGA	1920 1980 2040 2160 2220 2280 GCT GGG	STT CTG STT TTC TTC ACG ACG ACG ACG	ACCEPTED AGAGGCCGTG INTEGRACE OF AGAGGCCGTG INTEGRACE GGAGAAGCTG INTEGRACE CONTRAGE INTEGRACE INTEGRALE INTEGRACE IN	GGAGAGG GGGGAAG GGTGATA CGACGAG CCAGAAG CCAGAAG ATA AGA GAG CAC	CCTT GCCA GCCA GCCA GCCA GCCA GCCA GCCA	HITCG SCAAC SCAAC CTGG TGCG TGCG 232 232 CTT	AGG CGP CGP CGP CGP CGP CGP CGP CGP CGP C	TACA TACA TACA ATAC ATAC GAAG GGAA GTT AAG	CAAAGCTTTG CTAAAGGACG GTG GAAAAGCTG AGCAAGTACA AGG GCGAGAGGA GTCAAAATAC GCC GGGAGGATA GGCGACAGGG CGA TTCGGTTAC CGCAAGGAAG ACC TTGGCTGAG CGAAGGAAG ACC TTGGCTGAAG CCGAAGGAAG ACC CCA ATT GCC CCA GTT GAC GAG CAA AAG GCA GTA GAT	2	AGCTTA AGCTTA GGAGG GGTTA TGAA TGAA AAA	GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAC CALL	AAGTT AAGTTG AGGGC ACAAG ACAAG TGAGA TGAGA GAA GTT	ACCE AGGAGTTAC CGAAAGCTG AGCAAGTACG GIGACGICGA GAAGGCCGIG 1920 TCA AAGAAGTTAC CGAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980 ACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040 SCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCTGGAAC GGTGATAAGC 2100 STGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160 ACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCCAGCC 2220 ACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220 ATC GAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280 STTG GTTTGAGTGC TTGGCTGAAG CCGAAGGAAG TCTGCGCTA ATA AGA AAG GCT CAG AGA GTT AGC GAG CAA AGG GCA GTT GAC AGA CTT GCA CAG AGA ATT GAG AAA AAG GCA GTA GAT CTT GCA AAG CAC CTT GAG GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT	ATAGTCA ATAGTCA ATCCACG GTTGCCA CCGACGA CCGACGA CAGGTTG ATG ATG ATG ATG	SACAGA COTTG COTTG COCCAA COCC
くいつ プラグネググライン 手がひょうしゃ しょうしょ しょうしょ しょうしょうしょ しょうしんじょ しょうしん ないしゅ しんしんじしんしん			2160	T _T	GAG	CGAC	GIT	TACC	CGD	AGGG	CGAC	₽ 8	GGAT	GGGA	TC T	2000	TCAA	TGC	PATCE
TACATCGIGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160 GACCCGACGA AGCACAAGTA CGACGCAGAG TACTACATTG AGAAACCAGGT TCTCCCAGGT 222A			2100	AGC.	ATA	GGTG	AAC	CTGG	ပ္ပ	ATAC	CAAA	A GI	GAGG	GCGA	ပ္ပ	GTTG	AGAG	CCA	GTTG
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100 TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160 GACCGAGGA AGCACAAGGAA GGAGGCGAGAGA TACTACAATTG AGAACCAGGT TCTCCCAGGT 2220			2040	TI	CACC	TCC	CGG	CAAC	AGG	TACA	GGAC	A A	ATTT	AGGG	AC G	GATA	AGCA	ACG	ATCC
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100 TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160 GACCCGACGA AGCACACAGAGAAA TACTACAATACAAGA TACTACAAGA AGAACAAGA AACAAAGA AACAAAAAAAAAA			1980		BAAGC	GGAC	GCC	TICC	AGG	TACG	CAAG	G AG	AGCT	GAAA	AC O	AGTT	AAGA	TCA	ATAG
AGGATAGICA AAGAAGITAC CGAAAAGCIG AGCAAGIACG AGGITCCGCC GGAGAAGCIG 1980 GIGAICCACG AGCAGAIAAC GAGGAITIA AAGGACIACA AGGCAACCGG ICCCCACGII 2040 GCCGIIGCCA AGAGGIIGGC CGCGAGAGGA GICAAAAIAC GCCTGGAAC GGIGAIAAGC 2100 IACAICGIGC ICAAGGGCIC IGGGAGGAIA GGCGACAGGG CGAIACCGII CGACGAGIIC 2160			1920	3TG	3900	GAAC	CGA	ACGI	GIG	GACG	AAAG	5	CTLI	GAAG	CTT	GGTT	CGAG	AGG	ACGC
ACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920 ATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAACCGC GGAGAAGCTG 1980 ATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040 GTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100 ATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160				₹¥	\GCG7	GAT?	CGA	GGAG	ACT	CGTG	GAGG	T GI	AGAT	CTTG	GG A	3000	CAAC	TAA	AAGA
AAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860 ACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920 ATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAACTCCGCC GGAGAAGCTG 1980 ATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040 ATCCACG AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100 ATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160			1860	:		AGAC	GAL	755			5445		ָ כְּיִי	9 1 1) -			ACA	; ; ;
GGCAAGATAA CAACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAACTCCGCC GGAGAAGCTG 1980 GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100 TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160			1800	44	GAGC		E	としてして	ATG	AAGT	2 4 4 5	G A		CCEE	E	CGGC	AACG	5	TTCT

Figure 17M

(HMf-like) - ROD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 34)

CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSI V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 54 GCA GAG CAC CTT GAG GAA GCA AAG CAC GCA GGT AGA CTT ATA AGA AAG GCT GCA AAA AAG GCA GTA GAT CTT GCA AAG CA(GTT GAC AGA CAA GCA GCT AAG GTA CTT GCC CCA ATT CCA CAG AGA GTT AGC GAG GTT AAG GTC GAA GAA TTA GAG ATC ATT GGA ATG ATG AAA GCT AAG ACC GCT

240 300 CTTCTACGCC 120 ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG GAGGCACGGG CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC CAGCGATAAG GGACAAGATA CAAGCGCTAC GAGACCAGTT TAACCGCCGA AGTICCICGG TACCCTTCGC TTGAACCCTA GATTGAGTAC GACCGGACTT CATTGAGGAA GTCAAGAAGA TACTCATCCG CAGGACXXXC TGACATCTAC GAGTACGACA GTTCAGAAGA GGTTGAAAAG GCGAGTTTAA ACGATTCTGC AACTCTACTT CAGCAGTTAT CGGTTAAGCG CTCCTGAAGG GAGGTCTGGA AAGGAAAACG CGAGAGCATC ACGGTTGTAA

1260 1080 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740 1800 1920 1020 2040 2100 2160 1860 1980 900 TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA TCTCCCCTAC CTTCGATCTC AGCCTGGGAA CGGCCAGTCC GGCCAGAAGA TGTGAAGGAG CGTTTATGAA GGTCACATAC CCTCAGGAAG GGAGAACATA CGTCTCGCCG CGGCCACCGC GCTCCTCGAT CGGCTATGCA AAACCGTCAA AAAGAAGGCT CGAGTACGAG GGAGAAGCTG CGAGCCGAAG AGAGGAGAGG AAGGGAGTAC CTACAGCGAC AGACGAGGAA GAAGGCCGTG GGTGATAAGC CGATACCGTT CGACGAGTTC CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG GATAGCGAAA TCCCCACGTT TTGGCTGAAG CCGAAGGGAA CT //TAG 2325 ATAACTTGGA AGAACGTGGA GAGACCTCCT TCCTCCGTGT GACGGATACA CGCTTGAGGC AAATAACCAC AAGATGCGAA CTCGCTTAAT AACCTCGTTG AGTGGTTCCT AAAAGGAGCT GAGGGTTGTG TCACCCACAA CCCCACAGGT TCGAGAGGAA ACGGTTACTA CGGCCTGGGG TTAAGGTAAT CGCTTGAGCT ATGCGGTGAT GTGAGGCGTG ACTGGAGCGA GTGACGTCGA AGCAAGTACG AGGTTCCGCC AGGCAACCGG GCCCTGGAAC GGGATGGAAG GGCGACAACT TACGCTGAGG TACTCGATGG AAGCCCGATG TATGACGTTG CCCACATACA GCCCAGCTTT ATAAAGCGCT GCCCTCGGAA ATTTATCCCG AGCCTGCTTG GAAGGCCACG ATTGACCCGA AATACCTGGA GCCGATGCTG AAGAAGAAGT CTAAAGGACG AAGGACTACA GAAGTGAAGG GAGCCCGAGA TCAATCATCA AACAGCTACT GAGAGCGTAA AAGTACGGCT CTTCCGGGCG GGCGACAGGG GTCAAAATAC GGCCAGGGTG GAGGGAGATG TCCGATGGAG CAGCACTGGC GATCCTGGCA AGTCGCCCGC ATGCAAGGAA GATAGAGGAA AACCTACAAC AATAAACTTC GTTTGCCGTC GATAAACCTG GGCCCCGAAC CCTGTACCCC GGAGTGTGCA CAACGCCAAA CTTCGTCACG ACTTGAGATT CGAAAAGCTG GAGGGATTTA GGAGAAGGTT CTATGTAAAA TGAAGCTTTG TGGGAGGATA CTTCGGTTAC CGCGAGAGGA CTCTCTACCA ACGAGGAAGG TCTCGACGGA ACGLICICAL AAAAGCTCGG TGGGCGACAG ACCTTGAGAG AGGAGTTCCT ACTTCCCAGG AGAAGAAGAT GTTTGAGTGC TAAGACGGAC GTCAGCCGAA GGAATGAGCT ATGAAGGAGG ATTTAGATC ACAGAGAAGG GGTACTGCAA CCATCAAGGA TTTTGCCAC TCAAGTATAT AACGCGGCTT CGAGGGTTCT TCAAGGGCTC TTCTGAGAGC TCTCCCGCTC GGGCCATCAA CAACGCGCGG AAGAAGTTAC AGCAGATAAC AGAGGTTGGC AGCACAAGTA GACATTGAAA AGCTACGCCG CGGCAGAGCT GATACGCTCA GACCCGACGA GTTGACGTCG AAAGACCCGG AAGCGCTGTG ATTCAGAGGA TATCCTGTGA GCCTATGAGA GTGTACCTAG TTCTGCAAGG CAGAAGATAA AGGCCCCCT ATAACGATGA TACATCGTGC GCCGTCTTCG ACCGGCGAGA GAGCTTGGGA CTCTGGGACG TACAGGCAGA ACCGACGGAT ATGGAGTTCC GGCTTCTACA GGCAAGATAA GAGACGCAGG AGGATAGTCA GTGATCCACG GCCGTTGCCA STTGAGAGAA AGACAGGTTG

Figure 17N

(HMf-like) - Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	
GGT	GAA	AGA	
GCT	GAG	GGT	
AAG	CIT	GCA	
AGA	CAC	CAC	/
ATA	GAG	AAG	AGC
CTT	GCA	GCA	AAG
AGA	CLI	CTT	ATT
GAC	GTA	GAT	GCA
GTT	AAG	GTA	CIC
CCA	GCT	GCA	AAG
gcc	GCA	AAG	ATT
ATT	CAA	AAA	GAC
CCA	GAG	GCA	GAA
TTA	AGC	ATC	GIC
GAA	GTT	GAG	AAG
GGA	AGA	_	GTT
ATG	CAG	GCT	ACC
ATG	GCT	AAA	AAG

09	120	180	240	300	360	420	480	540	009	099	720	780	840	900	096	1020	1080	1140	1200	1260	1320	1380	1440	1500	1560	1620	1680	1740	1800	1860
AATTTTAAG	TATATATGCT	GAGACATGGA	AAGGGAAGTT	GGGCAAAATA	CAAGCGTTAT	CCTTGCCTTT	AATAATGATT	TTTGCCGTAT	TGTTAAAGAA	GTATCTCATA	ACATCCCGAA	AATCCACTTT	TGAGGCAGTT	TGCCGCTATA	TGCTAGGGCA	GCTGATAGGT	GTATCTTTA	AGAGTATAAA	AGGTTTGTGG	TACTCACAAC	TCCGATAGTA	GGACTTAATT	CGAAAAGAAA	CGGCTATATG	CGCATGGGGG	TAAGGTTCTT	ACTCATTAAA	GCTTGAGCTT	TGCAGTCATA	TTGGAGTGAG
CTATAATCCG	TTCAGCCCTA	TAAAGGGCGA	AATTTTTGGG	CAGCTATGCG	TACCCTTTGC	AGCTTAAGCT	AGGCCAGAT	AAAATATCGA	TTGTTCAAGT	TTGATTTGCC	GGGACAAAGA	TCAAGGGTAG	CGTATACGCT	CAGAGGAAAT	CAATGGAAGA	AGCTGGCAAA	TCGTGGAGTG	CTGATGAGGA	AGCCAGAAAA	CAATAATAGT	ACGATGTTGC	CCATACTCGG	TTGACCCGAT	ACAGCTATTA	AAAGCGTTAC	AGTTCGGCTT	AAAAGCCTGA	TTCCAGGTCT	AAAAGCGCTA	TAAGGAGAGA
GATGGCAAGC	GACCCTCATT	ATAAAGGCAA	GTCAGGAAAA	CAAGACXXXC	GAATATGACA	GGAGACGAGG	GAATTTGGAA	ATCACATGGA	ATAAAGCGTT	GGGGACAATT	GTCTTAGGAA	GCTGTGGAAA	AACCTCCCAA	AAATTAGGAG	GCCCAGTACT	ATGGAAGCTG	ACCGGCAACC	CCGAACAAAC	TATGTAAAAG	CTGTACCCTT	TGTAAGAATT	TTTATTCCCT	AAATCCACAA	TTGCTTGCAA	GAATGTGCTG	ATAGAGGAAA	ATACCCGGGG	AACTCCAAAC	TTTGTTACAA	TTGGAAGTAG
CATAACAAAA	AATAGAACTT	TATTGAGGAG	TGCAGTGAAA	CGAGCATCCC	TGACATTTAC	TCCCATGGAG	TGAGGGAGAT	GGCCAGAGTA	AAGAGAAATG	AACTTACAAT	AGTTCGGCTT	TGATAGTTTT	AAGGACGATA	AACCAAAAGC	GAAAAAACTA	ATTCTTCCCC	GAGATCAAGC	TGAACTTGCA	CCTGGGAGGA	TTTCCGCAGT	AAAAGAGGGC	CTTTCCGGGC	GAAGAAAATG	GGCTATTAAA	GTACTCGAAG	GATAAGAGAA	TTATGCCACA	AAACTACATA	GAGAGGATTC	AACAAGGGGC
ACACTGATTA	GGGAGTTTAA	ATGACTCCGC	GAGTGCTCGA	AGCTCATTTT	CAGCTGTGGT	AGGGCTTGAT	CGTTTTATCA	ATGAAGAAGA	TGTCCAATGA	ATGTGATAAT	AAAAGCTGGG	AGAGGATGGG	CAGTTGTGCG	TTTAGGAAA	AAGAAAGCAT	TCGGGAAGGA	GGGACGTCTC	ACGCGAGGAA	GAACAACTTA	TTTATTTGGA	ATACCCTTGA	TCTGCAAGGA	AAGATATAAA	ATAGGCAAAG	AGGCAAGATG	TAGAGATGAC	CTGACGGCTT	AGGAATTCCT	GCTTTTACTT	GCAGGATAAC
ATGATACTGG	AAAGAGAACG	CTTCTCAAAG	AAAACTGTGA	GAAGTCTGGA	AGGGAACATC	CTCATAGACA	GATATTGAAA	AGTTATGCCG	GTCGATGTTG	AAAGACCCCG	AAACGGGCAG	CCCAAGALTC	GATCTTTTCC	TATGAAGCAG	TGGGAAACAG	ACGTATGAGC	CAAAGTGTAT	AGGGTGGCAT	CGGCGCTTAA	GAAAATATCA	GTATCCCCAG	GGATATAGGT	GCAATGAGGC	ATGCTCGATT	GGGTATCCTA	AGACACTACA	TATGCGGACA	AAGAAAGCCA	GAGTATGAGG	GATGAAGAGG

2160 2040 2280 GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920 2100 2220 ACCGGGCACA AATTTTACTT AAACCAAGTT TTTAAGGTAT GGTTCCACTT AGCCATTGGC CAAAATACAG TAAAAGTGAA ACTACATAGA AGGACTACAA GCGATAGGGT GAAAGGAGGA CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325 GAGAAAATAG GCAAGAGGGA GGAAAGATAA GATCCGGACT TTTGGATACA AGGGATTTAA ATAGCTAAGG AGACTCAGGC AAAGGTTTTA CGATAGCAAA AAGACTTGCC TACTTAGGAT ACTCGAAGCG AGATGTTGTA GCAGATTACC CAAAGGGAGC ACACAAGTAC AAGTTGTTAG ATCCTAGAAA ATATCGTTCT TTATCCATGA AAAGCTGTAG GAAAAGCTTG CCTCATGTCG ATAATAAGCT ACAGAATACG TTGCCGGCAG

Figure 170

Vent DNA POLYMERASE - (HMf-like) FUSION PROTEIN

// Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 35)

CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

1020 720 540 9 900 AATAATGATT CTATAATCCG AATTTTTAAG GAGACATGGA GGGCAAAATA CAAGCGTTAT CCTTGCCTTT GCTGATAGGT TATATATGCT AAGGGAAGTT TGAGGCAGTT TGCTAGGGCA AGCCAGAAAA AGGTTTGTGG GTATCTCATA ACATCCCGAA TGCCGCTATA AGAGTATAAA TTTGCCGTAT TGTTAAAGAA AATCCACTTT TTCAGCCCTA AATTTTGGG TACCCTTTGC AGGGCGAGAT AAAATATCGA GGGACAAAGA AGCTGGCAAA TAAAGGGCGA CAGCTATGCG AGCTTAAGCT TTGTTCAAGT TTGATTTGCC TCAAGGGTAG CGTATACGCT CAGAGGAAAT CAATGGAAGA TCGTGGAGTG CTGATGAGGA GATGGCAAGC GACCCTCATT ATAAAGGCAA GTCAGGAAAA GGAGACGAGG GAATTTGGAA ATCACATGGA CCTGGGAGGA TATGTAAAAG GGGGACAATT GTCTTAGGAA GCTGTGGAAA ATTCTTCCCC ATGGAAGCTG ATAAAGCGTT AACCTCCCAA AAATTAGGAG GCCCAGTACT ACCGGCAACC CCGAACAAAC CAAGACXXXC GAATATGACA ACACTGATTA CATAACAAAA GGCCAGAGTA AATAGAACTT TATTGAGGAG TGACATTTAC TCCCATGGAG TGAGGGAGAT AAGGACGATA AACCAAAAGC GAGATCAAGC TGCAGTGAAA CGAGCATCCC AAGAGAAATG AACTTACAAT GAAAAAACTA TGAACTTGCA AGTTCGGCTT TGATAGTTTT GGGAGTTTAA TGTCCAATGA ATGTGATAAT TCGGGAAGGA ATGACTCCGC GAGTGCTCGA AGCTCATTTT CAGCTGTGGT AGGGCTTGAT CGTTTTATCA ATGAAGAAGA AAAAGCTGGG AGAGGATGGG TTTTAGGAAA GAACAACTTA CAGTTGTGCG AAGAAAGCAT GGGACGTCTC ACGCGAGGAA ATGATACTGG CTTCTCAAAG AAAACTGTGA AGGGAACATC CTCATAGACA GATATTGAAA TGGGAAACAG AAAGAGAACG GAAGTCTGGA AGTTATGCCG AAAGACCCCG AAACGGGCAG CCCAAGATTC TATGAAGCAG CAAAGTGTAT AGGGTGGCAT GTCGATGTTG ACGTATGAGC CGGCGCTTAA GATCTTTCC

1260	1320	1380	1440	1500	1560	1620	1680	1740	1800	1860	1920	1980	2040	2100	2160	2220	2280	
TACTCACAAC	TCCGATAGTA	GGACTTAATT	CGAAAAGAAA	CGGCTATATG	CGCATGGGGG	TAAGGTTCTT	ACTCATTAAA	GCTTGAGCTT	TGCAGTCATA	TTGGAGTGAG	AAGTGTTGAA	GGTTCCACTT	AGCCATTGGC	ACCGGGCACA	AATTTTACTT	AAACCAAGTT	TTTAAGGTAT	
CAATAATAGT	ACGATGTTGC	TITATICCCT CCAIACTCGG GGACTIAAIT	AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440	ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG	AAAGCGTTAC	GATAAGAGA ATAGAGGAAA AGTTCGGCTT	TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA	AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT	GAGAGGAITC ITIGITACAA AAAAGCGCTA TGCAGTCAIA	TAAGGAGAGA	TTAAAGAGGG	CAAAATACAG	TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC	CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA	GCGATAGGGT	ACTACATAGA	TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA	GG 2325 //
CTGTACCCTT	TGTAAGAATT	TTTATTCCCT	AAATCCACAA	TTGCTTGCAA	GAATGTGCTG	ATAGAGGAAA	ATACCCGGGG	AACTCCAAAC	TTTGTTACAA	TTGGAAGTAG	GAGGCTATAC	GAGAAAATAG	AGGGATTTAA	GCAAGAGGGA	GGAAAGATAA	GATCCGGACT	TTTGGATACA	TGGCTCAAGA
TTTCCGCAGT	AAAAGAGGC	TCTGCAAGGA CTTTCCGGGC	GAAGAAAATG	GGCTATTAAA	GTACTCGAAG	GATAAGAGAA		AAACTACATA	GAGAGGATTC	AACAAGGGGC	AAAGGTTTTA	AGATGTTGTA	GCAGATTACC	AAGACTTGCC	CAAAGGGAGC	ACACAAGTAC	ACTCGAAGCG	CTTAGATGCA
GAAAATATCA ITTATTIGGA ITTCCGCAGI CIGIACCCIT CAATAATAGI IACTCACAAC 1260	GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320				GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC	TAGAGATGAC	CTGACGGCTT	AAGAAAGCCA AGGAATTCCT	GAGTATGAGG GCTTTTACTT	GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG	ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA	AAAGCIGIAG AAGIIGIIAG AGAIGIIGIA GAGAAAAIAG CAAAAIACAG GGIICCACII	TTATCCATGA		ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT	ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT	TACTTAGGAT	CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
GAAAATATCA	GTATCCCCAG	GGATATAGGT	GCAATGAGGC	ATGCTCGATT	GGGTATCCTA	AGACACTACA	TATGCGGACA	AAGAAAGCCA	GAGTATGAGG	GATGAAGAGG	ATAGCTAAGG	AAAGCTGTAG	GAAAAGCTTG	CCTCATGTCG	ATAATAAGCT	ACAGAATACG	TTGCCGGCAG	CAAAGCTCAA

108 162 GCA GAG CAC CTT GAG GAA GCA AAG CAC GCA GGT AGA CTT ATA AGA AAG GCT GGT GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA CCA ATT GCC CCA GTT GAC AGA GAG CAA GCA GCT AAG GTA CTT GCA AAA AAG GCA GTA GAT CTT GGA GAA TTA C AGA GTT AGC C ATT GAG ATC C GTT AAG GTC C ATG ATG GGA GGT CAG AGA GCT ATT GAAA GCT ATT GAAG ACC GTT A

Figure 17P

Deep Vent- (HMf-11ke) DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 180 240 300 ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG SAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC AAAGAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
AGCTATGCTG	CCCTCTATCA ATGAGGAAGA	AGCCAAAGTC	GAGITCGCGA	AGGGGCCCAT	TATAATGATA	4 10 0 40 0 0
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	009
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	099
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	096
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTIGGIGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCT	GGGCCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGCCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG //		2328
			;			

54 108 162 CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GAG CAA GCA GCT AAG GTA CTT GCA AAG CAC CTT GAG GAA GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA GAA GAC ATT AAG ACC TGA ATG ATG GGA GAA TTA COGCT CAG AGA GTT AGC GAAAA GCT ATT GAG ATC GAAAA AAG ACC GTT AAG GTC G

FIGURE 17Q

(HMflike) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 38) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 37)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 GAG GAA GCA AAG CAC GCA GGT AGA ATA AGA AAG GCT GAG CAC CTT GAC ATT AAG CTC GCA ATT AAG AGC TGA CTT GCA GTT GAC AGA AAG GTA CTT GTA GAT CTT CCA GCT AAA AAG GCA GCA ATT GCC CAA CCA GAG GCA GAA TTA GCT ATT GAG ATC ACC GTT AAG GTC CAG AGA GTT AGC GAA GGA ATG AAG ACC AAA GCT

540 600 999 720 780 900 960 180 240 300 360 420 480 840 1080 1200 1320 1380 1020 1140 1260 1440 1500 ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG TGAGCCAAAG CCTCAGGAAG CGAGAGAAGG CTGGGAGGGG ATTGGATGAA GGGGAGGGAA GAGGCATGGG GAAGAGGTAC TATAATGATA TCTCCCGTAC GATAAGGGAG CTTTGACCTC AGTTTATGAG GGCCTGGGAG GGTAACGTAC CGGCCAGCCC TAACGTCTCA GGTTGGGCAC GAAGATGCTT CATTTACGCT GGATAAGATA GCTCGCATTI CTATCTAGTI TTAGACCTTA TAACCGCCGA AGTTCCTGGG GGGACGGTAG CCCTCGAGGC AGGATGCAAA AGAAAGGGCT ATTATGGGTA TTACGGCCTG CCGCAATAAG TTCCGTTCGC GGCGATGAAG AGCTCAAGTT AGGGCCCAT AAAAGATCGA TCCTCAAGGT TCGACCTTCC GAAGGATACA AGAGGGAGTA TAATCACCCA TCGCCCCAGA TCAAGAGGTT CAATCGAGAA AGATAGCTGA CAAGGTTAGT AGTGGTACCT GTAAGGAAGA AAGGAGCCGG GACAGAAACT GATTGATGAG GTTAGGAAGA GAGTTCGCGA ATAACGTGGA GGCGATTCTT TACGCTCACG TATTCAATGG AAGCCGGATG GCAAACAGCT GCAGAGAGCG CAGGACXXXC GAGTACGACA ATAAAGCGGT CCCCTGGGAA GAGATAAAGG CCAACATACA GCCCAGCTTT AACTTGGTGG CCCTCGATAA GAATACGATG CCCAGCCTGC TCTAAAGACC GGTTGAGTAC TGCCGAAAAG GATAAAGCTA GGAGAAAGTT AGTTGCAAAG CCCAATGGAG TTCAACTGGC GGCTCCAAAC GGGATACGTT AGGGTGTAGG TAAGGAGTGC TGAACACCCT TGACATCTTT CGAAGGGGAG AGCCAAAGTC GAGGGAGATG TACCTACAAC GACAGCGGTG GATAAACCTC GAGCCTGTAC TCCAATGGAA GGGGTTTATC GATGAAAGCT CAAAATCCTG GTIGGIACTG GCGAGTTTAA ATGACTCGCA GAATTATAGA CCGCAGTTAT ATGAGGAAGA TTTCCAGCGA AAAAGCTCGG TTGGGGATAT TTAGGAGAAC GACTGGAGAG TAGATTTCAG TGAACAGGGA AACGGGCAAT GGCTGTACTT AAGGCCTAAT CCCTCTATCA ATGTTATAAT GAAAGCCAAA GGGAGTTCTT TTTCTAGGTC GGAATGAATT GCTACGCTGG AGGACTTCCC TAAAAAGGAA CTCCTCAAAG GAGCTCGGTA GATTACAGGC GCAAAAGCCC AAAGAAAACG AGCTATGCTG AAGAGGGCCG GCAATCTTCG ACTGGAAAGG TAGTTTCCC AAGTTCTGCA AGGCAAGAAA AAGATAGTGA GAGGTATGGA AGAGAGCATT CTAATAGACA GACATAGAAA GTCGAGGTAG AAAGATCCCG ATGCAGAGGC TACCACGTGA CTGTGGGATG GCCTACGAGA CTAAGGGAGA CCGGATACGC

TATATAGAGT	TCGTAAGGAA	TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA	GGGCCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTGGA GCTTGAGTAC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CTAGTTATTT ACGAGCAGAT CACCAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	GITGCCGTGG CAAAAAGGIT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	TICGATCICA GGAAGCAIAA GIAIGACGCI GAGIAITACA IAGAAAAICA GGIITITACCI	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGICTIAC	ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA	AACATCAAGA	AGAAG TAA		2328

Figure 17R

JDF-3 - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 63)

V93R MOTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ACGCCCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGAAGAAAAAATCCTCGG CAGGTCTGTGGAGGTCTTGGGGTCCTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGGGTCATCGACATCTACGAGTACGACATACCC TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTQGAQATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAA **ACCCTCGGGAGGGACGGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA** aCgecGGTGGCTaCGTCaaGGAGCCGGAGCGGGACTGTGGGACAATATCGTGTGTATCTAGACTTTCGTAGTCTCTACTATCATCATCATCACCCACACGTCTCGCCAGATAC CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTCGATTACAGGCAACGGGCGATCAAGATTCTCGCCCAACAGCTACTACGGCTACTACGGCT GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAACCGCTGTGAGAAGCTTGGCCGTGAGCTTT **ACCTCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGGCTTTGAGAG** GGTCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC **ATGCCAGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAA<u>TGG</u>TCATCAGAGAGGAAGGAAAAGTTCGGTTTTAAAGTCCT** CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGGCTTGAGATAGTCAGGCGCG ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCTTACTACTTCT

actegagegagatagegaagaegagegaggegttttggaggegatacteaggeacgttgacgttgaagaggecgteagaattgteagggaagteacegaaaagetgageaa GITAAAAICCGGCCCGGAACTGTGATAAGCTACAICGTTCTGAAGGCTCCGGAAGGAIAGGCGACAGGCGATTCCCTTCGACGAGGTTCGACCGACGAAGCACAAGTACGATG CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCCGC GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGGTCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAg< GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

54 108 162 GCA AAG CAC GCA GGT AGA CTTAGA AAG GAA GAC AIT AAG CIC GCA AIT AAG AGC IGA GAG GCA CTT CIT AGA GAC GCT AAG GTA GCA GTA GAT CCA gcc GCA AAA AAG GAG CAA GCA CCA ATT TTA ATC GIC AGC GAG GTT GAA AAG ACC GTT AAG ATG GGA (CAG AGA C ATT AAA GCT

Figure 17S

(HMf-like) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 39)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 GCA GAG CAC CIT GAG GAA GCA AAG CAC GCA GGT AGA CIT ATA AGA AAG GCT GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC // CCA AIT GCC CCA GIT GAC AGA GAG CAA GCA GCT AAG GTA CTT GCA AAA AAG GCA GTA GAT CTT GAA TTA GAG ATC GIT AGC ATG ATG GGA CAG AGA AAA GCT ATT AAG ACC GCT

agcegegactetegegacaatatcetetatettagactttcetaqccfftcaatcataatcacccacaacetctceccăgatacectcaaccecgagegetet GACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAAACTCATGTCCTTGGAGATGGA CTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGGAGAAGGTGA GACGCTCTACCACGAGGAGAAGAGTTTGGAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGATAACCTGGAAGAAGATCGACCTTC NGGAGCTACGACGTTGCCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCCGGCTTCATTCCGAGCCTGCTGGAAAACCTGGTGGAGGAAAGGAAGATAAA agaaaagttcctcggcaggtctgtggaggtctgggtcctctacttcacgcacccgcaggacxxxccggcaatccgcgacaaataaggaagcacccgcgggtcatc CTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACTTC CGAGGTGAAGGGCAGGGTACACTTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGC CTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCCCGGCTCCAGCACCGGCACCTCGTCGAGTGGTTCCT

GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGGCCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATA CCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGAGGAAAAGTTCGGTTTTAAA GTCCTCTATGCAGACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACT GCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCG GTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGGGGGGCTCAAGGACTACAAGGCCACCGGCCC GCACGTAGCCATAGCGAAgcGTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGG CGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGC GGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAATT TACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Figure 17T

Pyrococcus furiosus DSM 3638, Archeael hostone (HMf-1) section 85 of 173 of the complete genome. ACCESSION No: AE010210 REGION: complement (8333..9082)

/product="pcna sliding clamp (proliferating-cell nuclear antigen)"

Nucleotide sequence (SEQ ID NO: 67) Amino acid sequence (SEQ ID NO: 68)

18 54	36 108	54 162	72	90	108 324	126 378	144 432	162
D GAC	I ATA	P CCG	N	I ATA	T ACA	CCA	A GCT	Z
I ATA	ი მვვ	r CTC	V GTT	L TTA	A GCA	L	D GAT	Ħ
L	D GAT	N AAT	g GGA	TACC	TACT	DGAC	K AAA	œ
CAA	E	L CTA	I ATT	DGAC	GGA	v GTT	L CTA	4
A GCC	T ACA	DGAC	T ACA	K AAG	CAA	E	v GTC	н
F TTT	v GTT	I ATT	e gaa	A GCA	I ATT	M ATG	E	Ĺτι
E	K AAA	L CTG	PCCA	K AAA	ACA	E	g GGA	×
K AAA	F TTT	v GIC	e gaa	G GGT	I ATA	GAA	LCTT	н
A GCA	A GCG	V GTT	v GTT	r Aga	E	v GTA	v GTT	Ø
G GGT	A GCC	r Aga	v GTT	K AAG	L TTA	D GAT	v GTA	Ω
E	E	S AGT	e gaa	L	F	I ATA	v GTT	ഗ
F	D GAT	P CCA	Y TAT	I ATC	N AAC	L CTA	K AAG	>
v GTA	I ATA	D GAT	K AAA	K AAG	E Gaa	CCC	A GCA	Ħ
I ATC	L TTA	M ATG	SAGC	k AAG	E	V GTT	TACT	ഗ
E	K AAG	₽ GCC	FTT	L	g GGA	R AGA	F	A
F TTT	S AGT	R AGG	I ATA	H CAC	A A A A	F	CCA	Ω
PCCA	A GCA	M ATG	S AGC	DGAC	K AAG	TACA	CTT	×
M ATG	TACC	s AGC	s TCA	M ATG	L	R AGA	E	>

486	180 540	198 594	216 648	234 702	250
AAT	T ACT	A GCA	E GAA	R AGA	
GAA	L	S AGC	D GAT	I ATT	
AGG	K AAG	K AAG	A GCC	Y TAC	* TGA
GCC	I ATA	T ACA	K AAG	Y TAT	E GAG
ATT	E GAG	e Gag	GGA	E GAG	GAA GAA
$\mathbf{T}\mathbf{T}$	V GTT	E GAG	L	M ATG	. V GTT
AAA 1	e Gaa	CAA	G GGA	CAA	R AGA
ATA	O CAG	V GTT	AAA	MATG	G P
AGC	T ACC	E GAG	V GTT	PCCC	A GCT
GAC	e gaa	I ATC	MATG	M ATG	r CTG
AGT	g GGA	D GAC	D GAC	E GAA	L CTA
GTG	E GAG	L TTG	S TCC	N AAT	F TTC
CTA	A GCA	L TTA	L	G GGA	ACA
TCT	K AAG	G GGA	Y TAT	F TTT	L CTT
၁၁၅	M ATG	E GAG	s AGC	K AAG	R AGA
GAT	I ATA	D GAT	V GTC	I ATA	g GGA
AAA	F TTT	E GAA	G GGA	T ACA	E GAA
TT	E SAA	ı ří	Y :AT	V FTT	D TAT

Figure 17U

(PCNA)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65) Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 66)

18	36	54
54	108	162
D GAC	I ATA	CCG
I		L
ATA	GGG	CTC
r	D	N
CTT	GAT	AAT
CAA	E	L CTA
₽	T	D
GCC	ACA	GAC
F	V	I
TTT	GTT	ATT
E	K AAA	r CTG
K AAA	F	V GTC
A	A	V
GCA	GCG	GTT
G	A	r
GGT	GCC	Aga
E	E	s
GAA	GAG	AGT
F TTT	D GAT	P
v	I	D
GTA	ATA	GAT
I	L	M
ATC	TTA	ATG
E	k AAG	A GCC
F	S	R
TTT	AGT	AGG
CCA	A GCA	M ATG
M	T	s
ATG	ACC	AGC

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L A GCC A GCC A r G A GCC ဗ္ဗဋ္ဌ R 23 L F V 3TG ဗ္ဗဋ္ဌ GGG L CTG X X CTC Y TAC E GAG F ACC R AGG V GTT CTC Y ი გე Ö E F GAA L Y TAT GGC GC s AGC r CTC CTT e gag я С R AGG T ACG 团 V GTG GCC GCC P CCG D GAT CCT R CGG CGG E GAG r CTG M ATG E GAG W TGG A GCC H P CCG A GCC CCC D L A K GAC CTG GCC AAG D GAC E DGAC A GCC s TCC CTT E V GTG W P TGG CCC M W ATG TGG A K GCC AAA H M CAC ATG L E CTG GAG LCTC မှ DGAC CCC V GTG LCIT \mathbf{r} GAG CHC DGAC ი წვვ A GCC A GCC R AGG S AGC P CCC CCC ဗ္ဗဗ္ဗ R CGG R CGG CIC E GAG S TCC A GCC E A GCC ₩ TGG (ဗ္ဗဗ္ဗ LCTT P R AGG gcc Gcc E CAC P CCC R CGG E r CTG L A K GCC AAA A E E GAG GAG AAG S F TTT V GTC ი მვვ P T ACC E GAG V GTC A GCC ი მმმ 고 5년 R CGC CIC T ACC E R CGG . ദദ് ი მცი E Y L R TAT CTC AGG A GCT N AAC A A A G F L L CTG S යිය A GCG ဗ္ဗင္ဗ A GCG S TCC CTT CŢĞ A GCC L s TCC GAG D GAC R AGG r CTT E GAG R AGG r CTT ი გე P K CCC AAG V A GTG GCC E D GAT A.A.G V GTG V GTG R AGG ဗ္ဗဗ္ဗ PCCT e GAG CCC ი მმმ GAC D GAC LCTG $_{
m TTT}$ L CTG T ACG TGG E A GCC GAA R AGG GAC F TTT s AGC ဗ ဗ A GCC D GAC R AGG r CTG E r CTG ₩ TGG r CTG A GCC GAA Γ V GTG L က ည v GTG A GCC r Agg E GAG AAC CTC LCTG F A GCC A GCC LCTG R AGG r CTG CIC Y ი მვი gcc Gcc GGC CGC E

R AGG IATC F AAC AAC I ATC A 3CC T ACC T ACG SAGT Y TAT IATC A GCC CAG R AGG L CTA DGAC CIG M ATG ACC r CTC 3 3 3 3 3 r Sign CTA R AGG GCC CCC AAC AAC ကို ည r CTG E 3AG ი მვვ r CTG AAC W A.A.G E 9 9 9 9 A GCC A S V GTC H L E Q CAG FITC CTT ج 60 ہے S AGC A T GCC ACG I ATC CCC ი ცცც ₽ GCC Y ව විට V GTG D GAC A GCC A GCG s TCC R T CGC ACC L L CTA A C Q CAG L TTG g GGC T ACC LCTC н САС R CGG × S TCC ဗ္ဗဋ္ဌ T ACG LCTA E E GAG s AGC r CTG DGAC အင္အင င္ပင္ပင DGAC T ACC P CCG ₽ GCC V GTC ₩ TGG CIC T ACG **₹** I M ATG H 闰 N Q T AAC CAG ACG (P L CAC K AAG GCC ი წმვ CAC r CTG r CTG s TCC GCC F Н Q N I CAG AAC ATC C E **₽** IATC CCC GGC r CTC R CG C E s TCG [tı GAC E $_{
m CTG}$ D GAC DGAC AAG V GTG M ATG F V GTC I ATT F A GCC V GTG CGG V GTC ဗ္ဗဋ္ဌ IATC v GTG ი მვი R AGG T Y ACC TAC I E GAG GAA ACC. GGC CGC සි දි r CTC R AGG ი მვვ A GCC Y TAC K AAG T N AAC F CIC L gcc Gcc GAG r CTG CAC GAG 团 H S AGC က္ခ A GCC E V GTC CAG CAG E A GCC CAG R AAG. CIC DGAT R CGG r CTC I ATA DGAC T ACG E F GG P ი მმც CTG r GGC S TCC r GGC CAG R V GTC V GTC F CGG K AAG င္ပင္ပဲ ဗ္ဗဋ္ဌ I ATC S AGC န ၂၀၁ CTC K AAG g GGC s AGC N AAC R GGG အင္ထင

Y V GTG စ ဗို E A ი მმმ G GGG R CGG E E CAG CIG ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC R CGG V GTC gcc B R AGG CIC MATG R AGG P CCC E GAG CCC CCC V GTC V GTC F N M TTC AAC ATG E G R GAG GGC AGG L CTA $_{
m F}$ r CTG A K E GCC AAG GAG P D CCA GAC K L AAG CTC D E V GTG R L E V GTG CAC gcc Gcc CIG V GTC Y E R M GAG CGC ATG M ATG R R CGC CGC V A GTG GCC CAG CAG W I E K T TGG ATT GAG AAG ACC D L M K L A GAC CTC ATG AAG CTG GCT CII ය ප A GCC gcc Gcc $_{
m L}^{
m L}$ R M AGG ATG A E GCG GAG ဗ္ဗဗ္ဗ A GCG E F E R GAG AGG (A GCC **&** 225 CŢĊ K CGG CGG V GTG gcc Gcc ი მვვ ACC K V AAG GTG K S AAG AGC T A ACC GCC E M GAA ATG k Aaa E V GTG CCA

e Gag H E V G I G GAG GTG GGG ATA GGG GGA GGC GGG CAT R G CGC GGC (V GTG L A V P L E CTG GCC GTG CCC CTG GAG ဗ္ဗဗ္ဗ DGAT I ATT E G K AAG V Y P GTG TAT CCC gcc Bcc * TAA CAT S TCC H GIC

W TGG

GAC

H

H

Figure 17V

Taq DNA polymerase- (PCNA) fusion protein

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 67)

0 0 0 // 36c 36c 66T

GTG V T S G M L P L F E P K G R V L L GTC ACT AGT GGG ATG CTC CTC TTT GAG CCC AAG GGC CGG GTC CTG

T ACC H A L K G L T CAC GCC CTC ACC TIC ſτι TAC CGC ACC H ద × ggg 4 CIG Ы CAC CAC Ħ Ħ GAC GGC r

K AAG CIC K S L AAG AGC CTC Q A V Y G F A CAG GCG GTC TAC GCC × > V GTG GAG CCG Д 团 999 Ö S R AGC CGG

CCC gcc Ccc K AAG A GCC GAC F TTT V GTC D A V I V GAC GCG GTG ATC GTG ය දෙය GAC GAG K AAG A L GCC CTC

CCA P P T CCC ACG gac Gac ස ප g GGC A GCG G G Y K GGG GGG TAC AAG Y gg A GAG CAC GGC BC F S TCC

ი მმმ r CTG CIC V D GTG GAC (r CTG GAG (A L I K GCC CTC ATC AAG Q L CAA CTC (ය ප ದ್ವದ್ಧ F TTT E D GAG GAC

r CTG s AGC gcc Bcc V L GTC CTG D D GAC GAC (gcg GAG Y ဗ ဗ္ဗ PCCG v GTC GAG CIC GGC CGC L A CTG GCG

X A GAC gcc Bcc L T CTC ACC R I CGC ATC Y E V TAC GAG GTC စ ဗ္ဗ GAG E K GAA AAG gcg K AAG A K GCC AAG

Y ი გგმ GAG GCC CCC CAC V L GTC CTC S D R I H TCC GAC CGC ATC CAC CIT r CTC CAG Y TAC D L GAC CTT

CAG L W E K Y G L R P D CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC TGG 4 S GGG P ACC L I CTC ATC

DGAC A GCC AGCC A ဗ ဗ္ဗ K AAG GAA L L CIT A r GTG FITC L L CTT CTG ი მვვ ACC R AGG ရ ရင္ပ K AAA V GTT CIC Y TAC CTC LCTG I ATC Н s AGC E K GAG AAG S E R TCC GAG AGG CGC GAG F GAA Y TAT s AGC CIC GGC CGC A D Y R A L T G D E S D N L P G GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG P CCT CGG P r CTG E GAG D GAT M ATG GGG R ი მვვ V GTG P CCG A I R GCC ATC CGG GAC CAC g CCG E GAC CCC L E E W CTG GAG GAG TGG g G C C A GCC L A K CTG GCC AAG GGG GTG P CCC A K GCC AAA D D GAC GAC CCC CIC ಶಿ W TGG u P W CCC TGG P M CCC ATG ' E GAG gcc gcc CIC GAC R CGG ရ ည ဗ္ဗဋ္ဌ K R R AAA AGG CGG E s AGC CTC Ø L K CTG AAG (GGG LCTT M M E GAG GCC CCC ^ဗ A GCC CAC CIT GCC CCC R K AGG AAG C R K CGC AAG s TCC F GAG A G E GCG GGG GAG V GTC ი მვი GCG G P S N T T CCT TCC AAC ACC CTC ₹ CCC LCTC CGG E GAG E GAG GGG R GGG PP GCG. F ဗ ဗ္ဗ D GAC K AAG LCTG s TCC ဗီဗ္ဗ A GCG LCTT K N L AAG AAC CTG (V D GTG GAC ' GC ATC GGG GAG AAG ACG A GCC E GAG LCTT D D L GAC GAT CTG r AGG LCTT ი მგვ 囟 K AAG (AAG E GAG V GTG R AGG စ ဗိမ္မ GAC E GAG F TTT LCTG Γ GCC Pp A GCC GAA CIC M ATG LCTG $_{
m TTT}$ s AGC ဗ္ဗဋ္ဌင A GCC GAC R AGG $_{
m L}^{
m L}$ GAA A H GCC CAC L P V GTG A GCC r AGG L CTG CTC CTC A GCC GIG FTC A GCC A GCC R AGG r CTG L CTG Y TAC

GCC GCC CTT

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IATC A GCC ACC. R VGTG A A C T ACG SAGT R AGG Y TAT I ATC I ATC **A** 320 E r CTC စ ဗ္ဗ E CTC R AGG CTA Q CAG DGAC r CTG CIT F G E GAG N AAC ကို ည r CTG E ပိုင္ပင္ r CTG R AGG ი GGG N AAC CTT A GCC gcc gcc F CTT v GTC ය දි CAC gga A E GAG CTT E GAG > G CCC g GGG A GCC Y TAC I ACG CCG V GTG DGAC CAG CTC MATG H r CTA gcc Gcc CIC r TTG GAG A GCC T ACC ဗ ဗ္ဗ L CTG R AGG E GAG ဗ္ဗဗ္ဗ s AGC CAC CIG GAC GGC BC ACG CTA န ၂၄၄ DGAC GAG A GCC A GCC ACC. IATC P CCG **₽** န ၂၃၄ V GTC W r CTC L F CTC TTT (E K GAG AAG 1 s TCC \mathbf{r} $_{
m L}$ r CTG ı rig T ACG CCC ත විසි CAC . ೧<u>೧</u>೧ က္ဆင္သ ည် უ ეტე V GTC A GCC o CAG IATC E A GCC V GTC K AAG V GTG GAG F DGAC N AAC GCT. R AGG a AAC GAG r CTG R AGG ggc IATC I ATT CIC V GTC CTT S TCC F CAG A GCC V GTG L E CTG GAA K T AAG ACC မှ သ R AGG CIT Y TAT E Y TAC ය දු CTC IATC R AGG Н ACC GGG gcc **4** 000 ပိုင္ပင္ပ ACC AAC F r CAG E E gcc gcc AGG BGG V GTG s AGC CAC CCC A GCC E GAG GAC T ACG EGAG E GAG K AAG L GAC LCTC CIC DGAT R I ATA R CGG K AAG GGC GC r CTG N AAC V GTG ය පු r G GGC GGC S TCC အင္လ CAG > gcc E s TCC 3 CTC K AAG I ATC ဗ္ဗ ₽ GCC 990 s AGC

IATC GCC GCC gg P Y V GTG ဗ္ဗဗ္ဗ E 3 P ი წმ ACC F ი მჭმ cgg w CAG CAG r GTG E EGAG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG CTA K AAG E GAG s AGC ය විව gcc Bcc V GTC AGG CIC M ATG V GTC gcc Gcc CAG E ပိုင္ပဲ က္က ည V GTC CAG R AGG E R AGG LCTA MATG FTTC L A GCG S TCC F TTT CGG $_{
m L}$ Y ၁၁၅ DGAC N AAC r. CTC E K AAG GCC 7 D GAC က္ဆင္သ F TTC GGC R E CCA K AAG င္ပင္ပင္သ L M ATG E H CAC E GAG V GTG A GCC V GTG LCTG V GTC R CGG A GCC IATT $_{
m L}^{
m L}$ Y M ATG M ATG V A GTG GCC F CAG CAG က် AGCT S ACC ဗ္ဗ ဗ္ဗ L CTG GAC k AAG E M ATG ggg G င္ပင္သင္တ V GTG ဗ္ဗဗ္ဗ CAG E င္ပင္သင္လ A GCC K AAG CTC A GCC L M R M AGG ATG E GAG Y ဗ္ဗဋ္ဌ A GCG TTC CAG GAG GGG GCC GCC A GCC IATT A GCG E CTC E W TGG F E DGAC A GCC R AGG CGG සි දියි V GTC E GAG GCC GCC CIC GAG ი მვვ ACC gcc Bcc က် ည ပ္ပင္ပ Y ස පි V GTG GIC E M GAA ATG E GAG s AGC K AAA V GTC F CCT V GTG GCC CGG ဗ္ဗဋ္ဌ AAC IATC K AAG V GTG K AAG T ACC CCA

W E ი მვვ I ATA ი მვვ ი მ<u>ვ</u>ვ g GGC V GTG g GGA E ဗ္ဗဗ္ဗ V GTG GGC BC L E CTG GAG ဗ္ဗဋ္ဌ DGAT GCC CCC IATT V GTG ဗဗ္ဗ E gcc Bcc K AAG L CTG က ည CAT s Icc Y TAT V GTG CTC

18 54	36 108	54 162	72 216	90	108 324	126 378	144 432	162 486	180 540	198 594	216 648
DGAC	I ATA	P CCG	N AAC	I ATA	T ACA	P CCA	A GCT	N AAT	TACT	A GCA	E
I ATA	ი მმც	r CTC	V GTT	L TTA	A GCA	L	D GAT	E GAA	L CTA	S AGC	D GAT
L	D GAT	n AAT	g GGA	TACC	TACT	D GAC	K AAA	r Agg	K AAG	K AAG	A GCC
CAA C	e gaa	L CTA	I ATT	DGAC	GGA	V GTT	r CTA	A GCC	I ATA	T ACA	K AAG
A GCC	₁ ACA	DGAC	T ACA	K AAG	CAA	e gaa	V GTC	I ATT	E GAG	E GAG	G GGA
F TTT	V GTT	I ATT	e gaa	A GCA	I ATT	M ATG	e gaa	F TTT	V GTT	E GAG	L CTT
E	K AAA	L	PCCA	K AAA	T ACA	E	G GGA	X AAA	e gaa	CAA	G GGA
K AAA	F TTT	v GTC	e gaa	GGT	I ATA	E GAA	r CTT	I ATA	Q CAG	V GTT	K AAA
A GCA	A GCG	V GTT	V GTT	R AGA	e Gag	V GTA	V GTT	S AGC	T	E GAG	V GTT
G GGT	A GCC	r Aga	v GTT	K AAG	L TTA	D GAT	v GTA	DGAC	E GAA	IATC	M ATG
E GAA	E	S AGT	E GAA	L CTA	F	I ATA	V GTT	S AGT	G GGA	D GAC	D GAC
F TTT	D GAT	CCA	Y TAT	I ATC	N AAC	L CTA	K AAG	V GTG	E GAG	L TTG	S TCC
V GTA	I ATA	D GAT	K AAA	K AAG	GAA	CCC	A GCA	L CTA	A GCA	L TTA	r CTC
IATC	L TTA	M ATG	S AGC	K AAG	E	V GTT	TACT	s TCT	K AAG	G GGA	Y TAT
E GAA	K AAG	A GCC	F TTT	L CTA	GGA	R AGA	F	A GCC	M ATG	E GAG	S AGC
F TTT	S AGT	r Agg	I ATA	H	к ААА	F TTT	P CCA	D GAT	I ATA	D GAT	V GTC
PCCA	A GCA	M ATG	S AGC	DGAC	K AAG	T ACA	L	K AAA	$_{ m TTT}$	e gaa	G GGA
MATG	T	S AGC	S TCA	M ATG	CTC	r Aga	e gaa	V GTT	E GAA	L	Y TAT

234	702	. r.)
œ	AGA		
н	ATT		
×	TAC	*	TGA
×	TAT	Ĺ	GAG
団	GAG	<u>[</u>	GAA
Σ	ATG	Λ	GTT
0	CAA	Q	AGA
Σ	ATG	ρ	် နည်
Д	CCC	6	gcī
Σ	ATG	Ė	CTG
田	GAA	ئ	ACA TIC CIA CIG GCT CCA AGA GIT
z	AAT	[S	TTC
ט	GGA	E	ACA
ſĿ,	TTT	ئ	CTT
×	AAG	þ	GGA AGA CTT
Н	ATA	۲	GGA
H	STT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	ני	SAT GAA
>	BLL	6	GAT

Figure 17W

Pfu DNA Polymerase (WT) -(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc totaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag cettecaatg gaaatteage ttteaagatt agttggaeaa eetttatggg atgttteaag agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac aggtggatte gttaaagage cagaaaaggg gttgtgggaa aacatagtat acctagattt tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc aataccaatg gaggggaag aagagctaaa gattettgee ttegatatag aaaceeteta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga

atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag aggogatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tentecenga tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagagta gatgctacct ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc gacactcaaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa

ATA CCG AATA ACA CCA GCT ACT GCA GAA AGA TTA 999 CTC GCA CTC GAT GAA CTA AGC GAT ATT ACA ATT GGA (GAC aaa aag aag GCC GCC CAA CIT ACA GAA GAT GAC CTA AAT GGA ACT TAC CTA GIT ATA ACA AAG TAT GAA CAA GAG GGA GTC GAA GLT GAG TTT ATT GAA GCA ATT ATG $_{
m LLL}$ GTT GAG ATG CTT AAA CTG ACA GAG CCA AAA GGA AAA GAA CAA GGA CAA AAA TTTATA GGT GTC GAA GAA CTT ATA GLI AAA CAG ATG GTA GCA ggg GTT GAG AGC ACC GAG GTT GTT AGA GTT CCC AGA GTT ပ္ပပ္ပ AAG TTA GTA GAA GGT GAT GAA ATC ATG ATG GAC CTA ATA (CCA AGT TAT GAA GAG CTA TIC GAC GAC AGT GGA GAA $_{
m LLL}$ GAT ATC AAC GTG GAG TTG ATA GAT AAG GTA GAA CIC AAA CCC GCA TTA CTA GGA GCA TTA ATG AGC AAG GAG AAG GGA GLL ACT TAT TTT CTT GAA ATC TCTggg GCA AGT AAG LLL CTA AGA GGA ATG GAG AGC AAG TIC ggg AGG ATA CAC ATA GAT GTC ATA GGA $_{
m LLL}$ AAA $_{
m LLL}$ CCA GAT AGC ATG
TCA AGC
ATG GAC
CTC AAG CCA AAA $_{
m LLL}$ GAA GGA ACA CTT GAA ACC GAA TAT GAA GTT

aagattgaga tgttcttgg

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

54	108	162	216	270	324	378	432	486	540	594	648	702	
GAC	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
ATA	999	CIC	GTT	TTA	GCA	CIC	GAT	GAA	CTA	AGC	GAT	ATT	
CTT	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ပ္ပင္ပ	TAC	
CAA	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ပ္သပ္သ	ATA	ACA	AAG	TAT	GAG
ggg	ACA	GAC	ACA	AAG	CAA	GAA	GIC	ATT	GAG	GAG	GGA	GAG	GAA
TTT	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TTT	GTT	GAG	CIT	ATG	GTT
GAG	AAA	CTG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
AAA	TTT	GTC	GAA	GGT	ATA	GAA	CIT	ATA	CAG	GLT	AAA	ATG	CCA
GCA	GCG	GTT	GTT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	CCC	GCT
GGT	ggg	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
GAA	GAG	AGT	GAA	CIA	TIC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TTG	TCC	AAT	TIC
GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CIA	GCA	TTA	CIC	GGA	ACA
ATC	TTA	ATG	AGC	AAG	GAG	GTT	ACT	TCT	AAG	GGA	TAT	$_{ m TTT}$	CTT
GAA	AAG	ပ္သင္ဟ	$_{ m TLL}$	CTA	GGA	AGA	$_{ m TTC}$	ggg	ATG	GAG	AGC	AAG	AGA
$_{ m TTT}$	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GIC	ATA	GGA
CCA	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	$_{ m LLL}$	GAA	GGA	ACA	GAA
ATG	ACC	AGC	TCA	ATG	CTC	AGA	GAA	GTT	GAA	CTT	TAT	GLL	GAT

tetaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cetecectat tttetetett atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc

taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagcc aagatgcaga gaataggcga tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt cettecaatg gaaatteage ttteaagatt agttggaeaa eetttatggg atgttteaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagotoca aacaagocaa gtgaagagga gtatcaaaga aggotcaggg agagotacac aggtggattc gttaaagagc cagaaaaggg gttgtggggaa aacatagtat acctagattt

tagagocota tatocotoga ttataattao coacaatgtt totocogata ototaaaatot tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat coctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg gaaggagoto gaagaaaagt ttggatttaa agtoototao attgacactg atggtotota tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag aggogatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggaggggg gatgctacct aaagtataaat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctcttt gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga TGA aagattgaga tgttcttgg //

FIGURE 17Y

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

// Nucleotide sequence (SEQ ID NO: 27) //Nucleotide sequence (SEQ ID NO: 28) Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 67) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) = GAA, V93E MUTANT: XXX

216 270 378 486 540 648 162 324 432 594 702 ATA ACA CCA ATA CCG AAC GCT ACT GCA GAA AGA 999 GCA CIC GII TTA CTC GAT GAA CTA AGC ATT GAT TAC GAT AAT GGA ACC AAA AGG AAG AAG gaa ACT GAC CIA GGA GAG ACA TAT GAA GAC CIA ggg AAG ATT GIT ACA ACA GAC AAG GIC GAG GAG GAG CAA GAA ATT GGA GAA GTT GAA TII ALT GCA ATG GAA GAG ATG ATT TTT GIT CTT CIG CAA AAA CCA AAA ACA GAG GGA AAA GAA CAA GGA AGA GIC GAA ATA ATA GAA CIT CAG AAA GGT GTT GAG AGC GIT CCC AGA GAG GIT GTT GTA GTT ACC ggg GGT AGA GIT AAG TTA GAT GTA GAC GAA ATC ATG ATG GAC GAG AGT GAA CTA ATA AGT GGA GAC GAA TIC GTT CTA GAT CCA AAG TTG TAT AAC GTG GAG JCC AAT ATA GAT AAA AAG GAA CCC GCA CTA GCA TTA CIC GGA ACA TIA AGC AAG CTT ATG AAG TAT GAG GTT TCT GGA ACT TIL ggg TTT AGA ggg GAG AGC AAG GGA TIC ATG AGT AGG ATA TII CCA GAT ATA GAT GTC ATA TII CAC AAA GCA ACA AGC AAA ACA GAA CCA ATG GAC AAG GGA CTT TIT GAA ATG CIC AGA CTT AGC TCA GAA GTT GAA TAT GTT

180 240 300 360 480 CTGTTATTAG GCTATTCAAA CATTTACGCT AAGGCATGGA TCTTCCATAC GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG CAAGCCTATT CCACTATTAG AGAAAAGTT AAAGAGATAC TCTTGCCTTC TATAATGATT TAACGGGGGA TTCCATTTGC TTAGACCATA GGGGAAGAAG AGCTAAAGAT AAGGCCCAAT AGTTTCTCGG AAAACATAGA ATGTGGATTA CATAACTGAA GAAGGAAAAC GTTAAGAAAA GAGTTTGGAA GATAGAACTT GTTGAGAAAA CAAGATXXXC GAATACGATA ATTACTTGGA GGAACATCCC GATAGAGCAT GATTGAAGAA TGTAGAGAAG GGACATCTTC ACCAATGGAG CGAAGGAGAA AGCAAAGGTG GAAAATTTAA TATCAAGCGA ATGATTCAAA AACTTTATTT AAGGCCTAAT ATGAAAATGA GAATTGTTGA CAGCAGTTGT CCCTCTATCA ATGATTTTAG AAAGAGAACG CTTCTCAGGG ACCGTGTGGA CTCATCGACA AGTTATGCAG GTTGAGGTTG AAGATTGTGA AGAGAACATC GATATAGAAA

AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTTAGCG	099
AAAAGGGCAG	AAAAACTTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
TATCATGTAA	TAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTATATGAA	840
GCAATTTTTG	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	900
AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	096
GAACTCGGGA	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTGTAG	AGTGGTTCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAGT	AGCTCCAAAC	AAGCCAAGTG	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACAGG	TGGATTCGTT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAC	1200
ATAGTATACC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCGATACTC	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAAGCGAT	AAAACTCTTA	GCAAATTCTT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCTG	GGGAAGAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACTATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAAG	1680
GCTCTAGAAT	TTGTAAAATA	CATAAATTCA	AAGCTCCCTG	GACTGCTAGA	GCTTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
GTAGCTGTTG	CAAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TICCIGGCII	AACATTAAAA	AATCC //		2328
// TGA						

Figure 17Z

PFU DNA POLYMERASE (V93 R OR E)-(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1020 1080 1140 1200 1260 1380 1500 1560 1440 540 900 900 840 960 CTGTTATTAG GCTATTCAAA ATAAGAGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA TIAGACCATA CATTIACGCT TICCATITGC AAAGAGAIAC CACTAGAGGC TGTATATGAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG AATACTCCTT TTATGGCTAT GGGAAGAAAG CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT TAACGGGGGA AAGGCATGGA AGCCTGGGAA GGCAACTTAT TGGACAACCT ACTTAGGAAA CCCTCGATTA TAATTACCCA CAATGTTTCT AAAGAAAAG AGAAAAGTT TCTTGCCTTC TATAATGATT ATATTAGCG CGAGCCCAAG TTTCGACTTG GTGGGAAAAC AGTAGGCCAC GTTAGAGGAA CAAGCCTATT TCTTCCATAC TATCAGGGAG Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) AATGAAGGAA ACTCAAGATC CTATAGAAAA TACGCCGACG AGATAGCAAA CCACTATTAG ATTACTTGGA AAAACATAGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT GGAGACTCAT TCGCATTCCC TCTACGGATA AGTTTCTCGG GGGGAAGAAG AGCTAAAGAT GAGTTTGGAA AAGGCCCAAT ACCATTGGAA GAGATGGAAG GAAGTCAAGG GAAGAATACA TACTCGATGG AAGATGCAAA CAAGATTAGT AGTGGTTCTT AAAGAGCCAG AAAAGGGGTT TCGCTCCTCA TGGGACATTT TTACTGCCTG GAAAAGTTTG GATTTAAAGT GTGAGGAAAT ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC GAAAATTTAA GATAGAGCAT GATAGAACTT GTTAAGAAAA TGTAGAGAAG GTTGAGAAAA CAAGATXXXC GAATACGATA CCAACATACA ATTCAGCTTT AACCTTGTAG AACTATGATA CCAAGTCTCT GCAAATTCTT GCTGAGAGCG AACTATCCCA GGAGGAGAAA V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, GATTAAATTA GATTGAAGAA GGAACATCCC GGACATCTTC ACCAATGGAG GACGGCTGTA GGAGAAGGTA ACCTTGAGAG AGTTGCCAAA TCCAATGGAA AAGCACAGGG TGGATTCGTT GGGATGCAAG TGGTTTTATA AAAACTCTTA CGAAGGAGAA AGCAAAGGTG TACTTATAAT TAGATTTTAG AGCCCTATAT TAAGGAGTGT AATAAATCTC GGAGCTCGAA AAGGCCTAAT AAAAACTTGG TAACAAGGAC TTTCAAGGTC GCTACACAGG TTAAGACAAA TTGTAAAATA ATGATTCAAA GAATTGTTGA AACTTTATT CAGCAGTTGT ATGAAAATGA GAAAGCCAAA AAGAATTCCT AGGACATCCC AAAAAGCGAT GATGGTACTG TAGTATGGAA GTCTCTATGC CCCTCTATCA TATCAAGCGA ACATTATAGT TAGGCGATAT TAAATCTTGA AGTGGAGAGA AAAGAGAACG CTTCTCAGGG CTCATCGACA TATCATGTAA GCCTACGAAA AGACAAAAGA GACTATAGAC GCTCTAGAAT SAAGGGTTTT ACCGTGTGGA AAGGATCCTG AAAAGGGCAG GAACTCGGGA AAGATTGTGA GATATAGAAA GTTGAGGTTG ATGCAGAGAA GCAATTTTTG TTATGGGATG CTCAGGGAGA ATAGTATACC CCCGATACTC AAGTTCTGCA TACATCGAGT GACACTGATG AGAGAACATC AGTTATGCAG GCAAAAGCAA

1980 2040 2100 2160 2220 2280 2328 TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860 AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC TGAAGAAGCT TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT GGGCAATTCT AGCTGAGGAA GGTTCTTCCA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG TTTGGAGACA ATACTAAAAC ACGGAGATGT TGGAGAACCA ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // CGATGGTCCA ATTAGCAATA GAATATTACA GTATGACGCA CTCGCAATAT ATGAGCAGAT AAGCTAGAGT CAAAGAAACT TACTTAGAGG AAAAGCACAA GGATATTGGA GTGAGAATAG SAAGGAAAAG GGATACATAG TACGATCCCA AAAGAAACTC GTAGCTGTTG GCGGTACTTA

540 162 216 270 324 378 432 486 594 648 702 ACT GCA ATA ACA CCA GCT AAT CCG GAA 999 GTT CIC TTA GAA CIC GAT GCA CTA AGC GAT ATT GAT AGG ggg TAC AAT GGA GAC AAA AAG ACC ACT AAG CTA CIA ATA GCC GAC GGA GTT ACA ACA ATT TAT GGA AAG AAG GAG GAG ACA GAC CAA ATT GAG GAA GTC GTT TTTATT GAA GCA ATT ATG GAA TTT GTT GAG CII ATG CIG CCA AAA ACA GAG GGA GGA GA AGA AAA GAA CAA ATA GAA ATA GIC GGT GAA CII CAG GTT GCA GLT GTT GAG AGC GLL CCC AGA GTA GTT ACC GAG ggg GAC ATG GTT AAG GAT GTA GAA ATC AGA TTA ATG AGT GAA GAC GAC CTA AGT GAA ATA GTT GGA CTA CCA GAT TAT ATC GTG TCC AAG TTG AAC GAG AAT AAA AAG CIC ATA GAT CCC GCA TTA GAA CTA GCA GGA ATC TTA ATG AGC AAG GAG GTT TCT AAG GGA TAT ACT $_{
m LLL}$ SCC AAG $_{
m LLL}$ CTA ATG AGC ggg GGA TIC GAG AGA AGA AAG AGT ATA GIC AGG GAT CAC AAA TTTCCA GAT ATA GCA AGC GGA ATG AAG ACA AAA $_{
m LLL}$ ACA CCA GAC GAA GAA CTT TCA AGC AGA TAT GTT ATG GAA GTT GAA CTT ACC

Figure 17AA

PPU DNA POLYMERASE (G387P/V93R OR E)-(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 67)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1260 1320 1440 1620 1680 1020 1080 1140 1200 1380 1560 1740 1500 840 900 9 900 or T) AAGGCATGGA AGATAGCAAA AGCCTGGGAA AGTAGGCCAC AATACTCCTT GGGAAGAAAG AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG CTGTTATTAG GCTATTCAAA CATTTACGCT CAAGCCTATT AGAAAAAGTT AAAGAGATAC TCTTGCCTTC TATAATGATT TCTTCCATAC TATCAGGGAG ATATTTAGCG CGAGCCCAAG TTTCGACTTG TGTATATGAA GGCAACTTAT TGGACAACCT ACTTAGGAAA TCAAAGAAGG GTGGGAAAAC CAATGTTTCT GTTAGAGGAA TTATGGCTAT CCTCTACATT AAAGAAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA TGAAGAAGCT G387P Mutant (CCN is the codon for Proline where N = C, G, A, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) TTAGACCATA GTTAAGAAAA TAACGGGGGA CCACTATTAG TTCCATTTGC GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TCGCATTCCC CACTAGAGGC AAGATGCAAA AGTGGTTCTT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCTACGGATA GTGAGGAAAT AGTTTCTCGG GGGGAAGAAG AGCTAAAGAT AAGGCCCAAT GAGATGGAAG GAAGAATACA CAAGATTAGT AAAAGGGGTT TAATTACCCA TCGCTCCTCA TGGGACATTT CTATAGAAAA TTACTGCCTG GACTGCTAGA GGTATGCAGT ACGGAGATGT AAAACATAGA GATTTAAAGT GAGATTGGAG ATGATITIAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CAAGATXXXC GAATACGATA CGAAGGAGAA GAGTTTGGAA GTTGAGAAAA ATTACTTGGA GGAGACTCAT AGTIGCCAAA TACTCGATGG AAAGAGCCAG GATAGAACTT ACCATTGGAA GAAGTCAAGG GGAGAAGGTA TACGCCGACG AACCTTGTAG CCCTCGATTA AACTATGATA CCAAGTCTCT AATGAAGGAA ACTCAAGATC GCTGAGAGCG GAAAAGTTTG GGAGGAGAAA ATACTAAAAC V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CCAACATACA ATTCAGCTTT GCAAATTCTT CATAAATTCA AAGCTCCCTG ATTCTTCGTT ACGAAGAGA TGGTTTAGAG ATAGTTAGGA GATAGAGCAT ATGATTCAAA GATTGAAGAA GGAACATCCC GGACATCTTC TACTTATAAT GACGGCTGTA AAGCACAGGG TGTAGAGAAG ACCAATGGAG AGCAAAGGTG GATTAAATTA AATAAATCTC TCCAATGGAA NGGATTCGTT GGGATGCAAG TGGTTTTATA TTTGGAGACA AGCCCTATAT AAAACTCTTA AACTATCCCA TAAGGAGTGT GGAGCTCGAA AACTTTATTT TTTCAAGGTC AGGACATCCC TTAAGACAAA TAAAAGAAGT CAGCAGTTGT ACCTTGAGAG GAAACGAAGT GAAAATTTAA GAATTGTTGA AAGGCCTAAT ACATTATAGT TAACAAGGAC GAAAGCCAAA GCTACACACC GTCTCTATGC CCCTCTATCA ATGAAAATGA TATCAAGCGA AAAAACTTGG TAGGCGATAT AAGAATTCCT TAGATTTTAG TAAATCTTGA AAAAAGCGAT GATGGTACTG TTGTAAAATA ATAAGAGGG TCATTACTCG AAGCTAGAGT TAGTATGGAA AAAGAGAACG CTTCTCAGGG AAGGATCCTG AGTGGAGAGA TTATGGGATG GCCTACGAAA AAGTTCTGCA AGACAAAAGA GACTATAGAC GCAAAAGCAA GTGAGAATAG AAGATTGTGA ACCGTGTGGA AGAGAACATC CTCATCGACA GATATAGAAA AGTTATGCAG AAAAGGGCAG TATCATGTAA GAACTCGGGA CTCAGGGAGA ATAGTATACC CCCGATACTC TACATCGAGT GACACTGATG GCTCTAGAAT AAAGAAACTC GTTGAGGTTG ATGCAGAGAA GCAATTTTG GAAGGGTTTT GAAGGAAAAG

2160 2220 2100 2280 2328 TTACATGAGT ATAAGGCGAT AGGTCCTCAC TAAAGCCAGG AATGGTAATT AGCTGAGGAA GGTTCTTCCA TACAGAAAGG AAGACCTCAG ATACCAAAAG GGCCAATTCT TGGAGAACCA TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // CAAAGAAACT AGCTGCTAAA GGAGTTAAAA ATTAGCAATA GAATATTACA CGATGGTCCA GTATGACGCA GGGATTTGGA CTCGCAATAT ATGAGCAGAT AACAAGACCA GGATATTGGA TACTTAGAGG AAAAGCACAA GTAGCTGTTG GGATACATAG TACGATCCCA GCGGTACTTA ACAAGACAAG

162 216 270 324 378 432 486 540 594 648 CCG ATA ACA CCA GCT AAT ACT GCA GAA AGA GTT AAC 999 TTA CTC GCA GAT GAA CTA ATT CTC AGC GAT TAC ggg GAT GGA ACC ACT GAC AAA AAG CTA AAT AGG AAG GAA CTA ATA GAC GTT ggg ACA AAG TAT GCC CAA GGA ACA ATT ACA GAC GAG GAA GAG GGA GAG AAG GAA GIC GAA ATT GTT ALT GAA TTT GCA GAG CLT ATT ATG GAA $_{
m LLL}$ GTT ATG CTG GAG AAA AAA CAA CCA AAA ACA GAG GGA GAA CAA GGA TTIATA ATA GTC GGT GAA CII CAG GTT AAA ATG GAA gag GTT GAG AGA GTA GLT AGC ACC GAG GTT GTT GGT AGA AAG GAT GTT TTA GTA GAC GAA ATC ATG ATG GAA GAA GAG CCA AGT GAA CTA GAC GAC CTA TIC ATA GTT AGT GGA ATA GAT $_{
m LLL}$ CTA TAT ATC AAC TTG AAT GCA AAG GTG GAG TCC GTA GAT GAA AAA CCC CTA GCA TTA CTC ATC TTA ATG AGC AAG GAG GGA GTT ACT TCT AAG TAT TTTGAA AAG ggg AAG TTTCTA GGA AGA $_{
m LL}$ ည္ဟ ATG GAG AGC AGA GGA AGT ATA TTT CCA CAC ATA GAT GIC ATG AGG AAA GAT GCA AAG CCA ACA ACA AGC GAC CTTAAA TIL GAA GGA AGC CTC AGA GAA CTTTCA ATG GTT ACC GAA TAT GTT GAT

Figure 17BB

(PCNA) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) or T) G387P Mutant (CCN is the codon for Proline where N = C, G, A, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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216
               270
                         378
                                   486
                                        540
                                             594
                                                   648
     162
                   324
                              432
                                                        702
         AAC
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                         CCA
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          GGA
                    ACT
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                    GGA
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                                   ggg
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                    CAA
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                                              CAA
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                                        AAG
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     ATG
          AGC
                                   AAA
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                                              GAA
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                         AGA
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1200 1020 1080 1140 099 780 840 900 960 480 540 600 CTGTTATTAG GCTATTCAAA CATTTACGCT TAACGGGGGA AAGGCATGGA CAAGCCTATT AGAAAAGTT AAAGAGATAC TCTTGCCTTC TATAATGATT TCTTCCATAC TATCAGGGAG ATATTAGCG CGAGCCCAAG TTTCGACTTG TGTATATGAA AGCCTGGGAA TGGACAACCT ACTTAGGAAA TCAAAGAAGG GTGGGAAAAC CAATGTTTCT GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC GGCAACTTAT TTAGACCATA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CCACTATTAG GGGGAAGAAG AGCTAAAGAT AAGGCCCAAT AGCAAAGGTG ATTACTTGGA AAAACATAGA CACTAGAGGC AGATAGCAAA CAAGATTAGT AAGCACAGGG AACCTTGTAG AGTGGTTCTT AAGCCAAGTG AAGAGGAGTA TICCALITIGC TTCTCAGGAT TCGCATTCCC GAAGAATACA AAGATGCAAA AAAGAGCCAG AAAAGGGGTT GAGATGGAAG TAATTACCCA GAATACGATA TACGCCGACG ATGTGGATTA CATAACTGAA GAAGGAAAAC GTTAAGAAAA GAGTTTGGAA ATAAAGAGAT GGAGACTCAT CCAACATACA TACTCGATGG TCCAATGGAA ATTCAGCTTT AGCCCTATAT CCCTCGATTA GATAGAGCAT GATAGAACTT CAAGATXXXC ACCATTGGAA GAAGTCAAGG GAGAGAGATG GATTGAAGAA GGAACATCCC ACCAATGGAG GATTAAATTA GGAGAAGGTA NGGATTCGTT GGACATCTTC TACTTATAAT GACGGCTGTA AATAAATCTC AGTTGCCAAA AGCTCCAAAC CGAAGGAGAA GAAAATTTAA ATGATTCAAA GAATTGTTGA CAGCAGTTGT CCCTCTATCA ATGAAAATGA TATCAAGCGA ACATTATAGT TAACAAGGAC ACCTTGAGAG AAGAATTCCT TTTCAAGGTC GCTACACACC CCCGATACTC TAAATCTTGA AACTTTATTT AAGGCCTAAT AAAAACTTGG TAGGCGATAT GAAAGCCAAA GAAACGAAGT TAGATTTTAG AGTTATGCAG ATGATTTTAG ATAGTATACC AAAGAGAACG ACCGTGTGGA GATATAGAAA GTTGAGGTTG AAGGATCCTG TATCATGTAA GAACTCGGGA TTATGGGATG CTCAGGGAGA CTTCTCAGGG AAGATTGTGA AGAGAACATC CTCATCGACA AAAAGGGCAG ATGCAGAGAA GCAATTTTG AGTGGAGAGA GCCTACGAAA

1440 1620 1740 1800 1860 TITGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 2100 2160 GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 AAAGAAAAAG 1680 CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 2040 TGGAGAACCA GGTTCTTCCA 2220 GGGCAATICT AGCIGAGGAA CTATAGAAA AATACTCCTT GGGAAGAAAG CCTCTACATT GCTTGAATAT TGAAATTGCA AGGTCCTCAC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA AATGGTAATT AATAGATGAA TTATGGCTAT TICCIGGCIT AACAITAAAA AAICC //TAG AACTATCCCA GGAGGAGAAA GTGAGGAAAT ATAAGGCGAT TAAAGCCAGG GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CATAAATTCA AAGCTCCCTG GACTGCTAGA GAGATTGGAG TCTACGGATA TTACTGCCTG GGTATGCAGT TAAGGAGTGT GCTGAGAGCG ACGAAGAAGA ATAGTTAGGA TTACATGAGT AGCTGCTAAA GGAGTTAAAA GTATGACGCA GAATATTACA AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC AAAACTCTTA GCAAATTCTT ATTAGCAATA TGGTTTAGAG AACAAGACCA CGATGGTCCA ATTCTTCGTT AATACAAAAG AGGACATCCC ACAAGACAAG TCGGCCTAAC TAAAAGAAGT AAGCTAGAGT ATGAGCAGAT AAAAAGCGAT TTGTAAAATA ATAAGAGGGG TCATTACTCG CAAAGAAACT GATGGTACTG TAGTATGGAA GTCTCTATGC TACTTAGAGG TACGATCCCA AAAAGCACAA GGATATTGGA TACATCGAGT GCGGTACTTA GACTATAGAC GAAGGAAAAG AAAGAAACTC AAGTTCTGCA GTGAGAATAG CTCGCAATAT GTAGCTGTTG GGATACATAG SCAAAAGCAA GACACTGATG GCTCTAGAAT GAAGGGTTTT

Figure 17CC

(PCNA) -PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 31) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 32)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) D141A/E143A Mutant (GCN is the codon for alanine where $N=C,\ G,\ A,$ or T)V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 216 CTC CCG GTT AAC GGG ATA ATA GAC CHI GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GCA AAA GAG TTT GCC CAA GTT ACA GAA GCG TTT AAA GTA TTT GAA GGT ATA GAT GAG GCC GAT TTA GAA ATC AGC ATG AGG GCC ATG AAG CCA TTT GCA AGT ATG A

540 648 378 432 486 594 702 ACA GCT AAT ACT GAA GCA GCA GAT GAA CTA GAT ATT CIC AGC TAC AAA AGG AAG AAG ပ္သပ္ပ GAC GGA ACT GAA GAG // CIA ATA ACA GAG TAT GTT gg GGA AAG GAG CAA GAG AAG GAA GIC ATT ATG TIIATG GTTATT GAA GIT GAG CTTACA CAA GAG AAA GAA CCA AGA GGA CAA GGA ATA ATA ATG GAA CTT CAG GIT AAA GAG CCC AGA GTA GTT AGC ACC GAG GTT GCT CTG AAG ATG TTA ATG GAT GTA GAC GAA ATC GAC GAA CTA CHE ATA GTT AGT GGA GAC AAC GTG AAT TIC AAG TCC GAG TIG AAG ACA GAA GCA TIA GGA CCC CTA GCA CIC AAG GAG AAG GGA CTT TAT ACT TCT TTT GTT ATG AAG AGA CTA GGA TIC AGC AGA GCC GAG CAC AAA TTT GAT ATA GAT GTC ATA GGA CCA AAG GGA GAA GAC TTT ACA ACA CII AAA GAA GAT GAA TAT GTT AGA GAA GIT CIT

GCTACACA GIT GGAITCGIT AAAGAGCCAG AAAAGGGGGIT GIGGGAAAAC 1200 TITCAAGGIC AAGCACAGGG AACCITGIAG AGIGGIICII ACITAGGAAA 1080 GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 TAGATITIAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTITCT 1260 1320 1380 1440 //ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 900 960 540 009 999 840 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC AGTIGCCAAA TACTCGAIGG AAGAIGCAAA GGCAACTIAI CGAGCCCAAG GAAGAATACA TTTCGACTTG TGTATATGAA TACGCCGACG AGATAGCAAA AGCCTGGGAA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAG CCACTATTAG AGAAAAGTT CAGCAGTIGT GGACATCTIC GAATACGATA TICCATTIGC AAAGAGATAC AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC IACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT TCTTCCATAC TTCTCAGGAT TATCAGGGAG ATATTTAGCG AATACTCCTT CCAACATACA CACTAGAGGC ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TACTIATAAT GGAGACTCAT TCGCATTCCC GATTAAATTA ACCATTGGAA GAGATGGAAG CTATAGAAAA CAAGATXXXC GAGAGATG ATAAAGAGAT GACGCTGTA GAAGTCAAGG TTAAGACAAA AATGAAGGAA ACTCAAGATC AACTITATIT GGAACAICCC GAAAGCCAAA GGAGAAGGTA TAACAAGGAC AATAAATCTC ACCTTGAGAG CCCTCTATCA TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT CCCGATACTC AAGATTGTGA CTCATCGACA AGTTATGCAG GAACTCGGGA GCCTACGAAA ATAGTATACC AGACAAAAGA AGAGAACATC GCNATAGCNA GTTGAGGTTG AAGGATCCTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCAATTTTTG AGTGGAGAGA TTATGGGATG CTCAGGGAGA AAGTTCTGCA GACTATAGAC ACCGTGTGGA GCAAAAGCAA

1740 1860 1920 1980 2100 2280 2040 2220 2160 AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG GAGATTGGAG TGAAATTGCA AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT GCTTGAATAT AATAGATGAA TAAAGCCAGG AATGGTAATT AGCTGAGGAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG AGGTCCTCAC GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG GACTGCTAGA GGTATGCAGT ATAAGGCGAT GGCCAATTCT ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // CATAAATTCA AAGCTCCCTG TGGTTTAGAG ATAGTTAGGA TTACATGAGT AGCTGCTAAA GGAGTTAAAA ATTCTTCGTT ACGAAGAAGA CGATGGTCCA ATTAGCAATA AACAAGACCA TAAAAGAAGT GTCTCTATGC CAAAGAAACT TTGTAAAATA ATAAGAGGG TCATTACTCG ATGAGCAGAT TACTTAGAGG TACGATCCCA AAAAGCACAA GGATATTGGA GAAGGAAAAG GTGAGAATAG GGATACATAG SACACTGATG GAAGGGTTTT CTCGCAATAT GTAGCTGTTG SCGGTACTTA GCTCTAGAAT

Figure 17DD

- (PCNA) fusion protein PFU DNA POLYMERASE (D141A/E143A/V93R OR E)

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA TTAGACCATA CATTTACGCT TAACGGGGGA AAGGCATGGA AGAAAAAGTT GGACATCITC GAATACGATA TICCATITGC AAAGAGATAC TCTTGCCTTC TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CGAAGGAGAA GAGTITGGAA AAGGCCCAAT TATAATGAIT CCACTATTAG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT GATAGAGCAT GATAGAACTT GTTAAGAAAA CAAGATXXXC GATTGAAGAA GGAACATCCC GAAAATTTAA ATGATTCAAA GAATTGTTGA CAGCAGTTGT AAGGCCTAAT CCCTCTATCA AACTTTATTT CTCATCGACA GCNATAGCNA AAAGAGAACG CTTCTCAGGG ACCGTGTGGA AGAGAACATC AAGATTGTGA

GTTGAGGTTG T	ATGAAAATGA TATCAAGCGA	AGCAAAGGTG GAGAGAGATG	ATTACTTGGA ATAAAGAGAT	AAAACATAGA TTCTCAGGAT	TCTTCCATAC TATCAGGGAG	
8	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTAGCG	099
\$	AAAAACTTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
8	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
4	TAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTATATGAA	840
4	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	006
ы	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	096
¥	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
Ξ	<i>LTTCAAGGTC</i>	AAGCACAGGG	AACCTTGTAG	AGTGGTTCTT	ACTTAGGAAA	1080
7	GAAACGAAGT	AGCTCCAAAC	AAGCCAAGTG	AAGAGGAGTA	TCAAAGAAGG	1140
5	GCTACACA GI	GTT_GGATTCGTT	. AAAGAGCCAG	HAPAGGGGTT	CTGGGAAAA	1200
¥	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGITICI	1260
7	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
5	AGGACATCCC	TGGTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
	LTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
\mathbf{a}	AAAAAGCGAT	AAAACTCTTA	GCAAATTCTT	TCTACGGATA	TTATGGCTAT	1500
4	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCTG	GGGAAGAAAG	1560
¥	FAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
꿉	STCTCTATGC	AACTATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAG	1680
잂	<i>LTGTAAAATA</i>	CATAAATTCA	AAGCTCCCTG	GACTGCTAGA	GCTTGAATAT	1740
	ATAAGAGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
77	<i>PCATTACTCG</i>	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
×	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
\Rightarrow	TAAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
잂	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
\$	CAAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
\mathcal{L}	FACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
\$	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTCCA	2220
77	GGATATTGGA	GGGATTTGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAAG	2280
8	rcggcctaac	TTCCTGGCTT	AACATTAAAA	AATCC //	,	2328

54	108	162	216	270	324
GAC	ATA	ညည	AAC	ATA	ACA
ATA	පියිය	CIC	GTT	TTA	GCA
CTT	GAT	AAT	GGA	ACC	ACT
CAA	GAA	CTA	ALT	GAC	GGA
၁၁၁	ACA	GAC	ACA	AAG	CAA
$_{ m TTT}$	GTT	ALT	GAA	GCA	ATT
GAG	AAA	CIG	CCA	AAA	ACA
AAA	TTT	GIC	GAA	GGT	ATA
GCA	ggg	GIT	GIT	AGA	GAG
GGT	ggg	AGA	GIL	AAG	TTA
GAA	GAG	AGT	GAA	CTA	$_{ m TTC}$
TTT	GAT	CCA	TAT	ATC	AAC
GTA	ATA	GAT	AAA	AAG	GAA
ATC	TTA	ATG	AGC	AAG	GAG
GAA	AAG	ggg	TTT	CTA	GGA
$_{ m TTT}$	AGT	AGG	ATA	CAC	AAA
CCA	GCA	ATG	AGC	GAC	AAG
ATG	ACC	AGC	TCA	ATG	CIC

80	7	9	0	4	œ	7	
37	43	48	54	594	64	70	
CCA	GCT	AAT	ACT	GCA	GAA	AGA	
CTC	GAT	GAA	CTA	AGC	GAT	ATT	
GAC	AAA	AGG	AAG	AAG	ggg	TAC	TGA
GTT	CTA	ပ္သင္ဟ	ATA	ACA	AAG	TAT	GAG
				GAG			
						ATG	
GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
GAA	CTT	ATA	CAG	GTT	AAA	ATG	CCA
GTA	GTT	AGC	ACC	GAG	GTT	CCC	GCT
GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
ATA						GAA	
CTA	AAG	GIG	GAG	TIG	TCC	AAT	TIC
CCC	GCA	CIA	GCA	TTA	CIC	GGA	ACA
GTT	ACT	ICI	AAG	GGA	TAT	$_{ m LLL}$	CTT
AGA	TIC	ပ္သင္ပ	ATG	GAG	AGC	AAG	AGA
TTT	CCA	GAT	ATA	GAT	GIC	ATA	GGA
ACA				GAA			
AGA						GTT	GAT

Figure 17EE

KOD DNA POLYMERASE - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 540 009 099 840 CAAGCGCTAC CTGTCATAAG AATTTTCAAG GAGGCACGGG GAGACCAGTT GGACAAGATA GCTCGCCTTC CCTTATGATA TCTCCCCTAC TGTGAAGGAG CTATCTGAAA CGAGCCGAAG CTTCGATCTC ACCEGCEAGA ACCITEAGAG AGICECCEC IACICGAIGG AAGAIGCGAA GGICACAIAC TTGAACCCTA CTTCTACGCC CGTTTATGAA AGCCTGGGAA GLUTAMIC ACID) TAACCGCCGA AGTTCCTCGG CAGCGATAAG AAATAACCAC TACCCTTCGC TCCTCCGTGT CGCTTGAGGC AGGGGCCAAT AGAACGTGGA TCGACTTCGC GACGGATACA GGCGACGAGG AGCTGAAAAT GGGATGGAAG TACGCTGAGG V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC GCGAGITIAA GATIGAGIAC GACCGGACII GTCAAGAAGA GTTCAGAAGA CAGGACXXXC GAGTACGACA GAGTTCGCCG ATAACTTGGA ATAAAGCGCT GGCGACAACT GCCCTCGGAA GAAGTGAAGG CCCACATACA GAGGGAGATG CATTGAGGAA GGTTGAAAG AACTCTACTT TACTCATCCG TGACATCTAC GCCAATGGAA GGCCAGGGTG TGAGGGCGAG AACCTACAAC GGAGAAGGTT AATAAACTIC GTTTGCCGTC GATAAACCTG CGGTTAAGCG CAGCAGTTAT AGGGATTAGT AAAAGCTCGG GTCAGCCGAA TCTCGACGGA ACGTTCTCAT ACGATTCTGC CTCTCTACCA ACGAGGAAGG TGGGCGACAG TAAGACGGAC CTCCTGAAGG AAGGAAAACG GAGGTCTGGA CTCATAGACA AAAGACCCGG GCCGTCTTCG ACGGTTGTAA GTTGACGTCG AAGCGCTGTG ATTCAGAGGA TATCCTGTGA CGAGAGCATC GACATTGAAA AGCTACGCCG

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           CCTCAGGAAG
                        GGCCAGAAGA
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                                                   CGICICGCCG
                                                              CGGCCACCGC
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CGGCCAGTCC
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                                    GAGGGTTGTG
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            TCTCCCGCTC
                        GGAATGAGCT
                                      ATGAAGGAGG
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                                                                                                                 AGGCCCCCT
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4)	70	16	21	27	32	37	43	48	54	52	64	7	
GAC	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
ATA	ggg	CIC	GTT	TTA	GCA	CIC	GAT	GAA	CTA	AGC	GAT	ATT	
CII	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ggg	TAC	TGA
CAA	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ပ္သင္ပ	ATA	ACA	AAG	TAT	GAG
ggg	ACA	GAC	ACA	AAG	CAA	GAA	GIC	ATT	GAG	GAG	GGA	GAG	GAA
$_{ m LLL}$	GTT	ATT	GAA	GCA	ATT	ATG	GAA	$_{ m TTT}$	GTT	GAG	CIT	ATG	GTT
GAG	AAA	CIG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
AAA	TTT	GIC	GAA	GGI	ATA	GAA	CTT	ATA	CAG	GIT	AAA	ATG	CCA
GCA	ggg	GIT	GIT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	CCC	GCT
GGT	ggg	AGA	GIT	AAG	TIA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	c_{IG}
GAA	GAG	AGT	GAA	CTA	TIC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
$_{ m LLL}$	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TIG	TCC	AAT	TIC
GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CIC	GGA	ACA
ATC	TTA	ATG	AGC	AAG	GAG	GTT	ACT	TCT	AAG	GGA	TAT	$_{ m LLL}$	CIT
GAA	AAG	ggg	TTT	CTA	GGA	AGA	TIC	gcc	ATG	GAG	AGC	AAG	AGA
$_{ m LLL}$	AGT	AGG	ATA	CAC	AAA	$_{ m TTT}$	CCA	GAT	ATA	GAT	GTC	ATA	GGA
CCA	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	$_{ m LLL}$	GAA	GGA	ACA	GAA
ATG	ACC	AGC	TCA	ATG	CIC	AGA	GAA	GTT	GAA	CTT	TAT	GTT	GAT

24 78 32 86

94 94 84

08 62 16 70

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) = GAA, V93E MUTANT: XXX

162 216 270 324 378 432 486 540 594 648 ATA AAC ATA ACA CCA GCT AAT ACT GCA AGA GAA 999 GTT TTA GCA GAA CTA AGC GAT ATT CIC CIC GAT AAG TAC GAT GGA GAC AGG AAG ggg ACC ACT AAA AAT GAG CTA ACA CIA ပ္ပင္ပ ATA AAG GTT TAT GAA GAC GGA ACA ATT GAG GGA ACA GAA GAG AAG GAG GAC GAS GIC ATT GTT GAA ATG GAA $_{
m TTT}$ GAG CII ATG GCA ATT GIT ATT GAG AGA CTG CCA ACA AAA GAA CAA GGA CAA AAA AAA GGA GAA GGT ATA ATA GAA CAG GTT AAA GTC CTT ATG GCG GII AGA GAG GTA AGC GAG GTT င္ပင္ပ GTT GTT ACC ggg AAG GAT GAC GAA ATC ATG ATG CIG AGA GTT TTA GTA CTA GAA GAA CTA GAC GAC AGT ATA GTT AGT GGA GAG CCA GAT AAC CIA AAG GIG GAG TTG ICC AAT TAT ATC ACA AAA AAG GAA CCC GCA GGA ATA CTA GCA CTC GAT TTA CTT AGC GGA TAT TTA ATG AAG GAG GII ACT TCT AAG TTTggg AAG AGA AAG LLL CIA TIC ATG GAG AGC GGA AGA GCC ATA GIC ATA GGA AGT AGG CAC AAA LLL CCA GAT ATA GAT GCA ATG AGC GAC AAG ACA CTT AAA $_{
m TTT}$ GAA GGA ACA GAA AGC TCA GTT GAA TAT GTT GAT ATG AGA GAA CTT ATG CTC

300 420 ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG CTTCTACGCC GAGGCACGGG GAGACCAGTT CAAGCGCTAC GGACAAGATA GCTCGCCTTC TAACCGCCGA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT TTGAACCCTA GTTCAGAAGA AGTTCCTCGG TACCCTTCGC CAGCGATAAG GATTGAGTAC GACCGGACTT CATTGAGGAA GTCAAGAAGA GAGTACGACA CAGGACXXXC GGTTGAAAAG CAGCAGTTAT TGACATCTAC TACTCATCCG ACGATTCTGC CGGTTAAGCG GCGAGTTTAA AACTCTACTT AAGGAAAACG CTCCTGAAGG GAGGTCTGGA CTCATAGACA ACGGTTGTAA CGAGAGCATC

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CCTTATGATA
                               TGTGAAGGAG
                                                             CGAGCCGAAG
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              GGCCAGGGTG ATAACTTGGA AGAACGTGGA
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 AGGGGCCAAT
                              TCCTCCGTGT
                                              TCGACTTCGC
                                                             AATAAACTTC GCCCTCGGAA GGGATGGAAG
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 TGAGGCGAG GAGTTCGCCG
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                                                                                                                                                                                                                                                                                                                                                                            TGAAGCTTTG
                                                            AAAAGCTCGG
                                                                                                                                                                                                                    GATACGCTCA ACAGAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTGAGTGC
 CTCTCTACCA
                                                                                                                                                                                                                                   ACTTCCCAGG
                                                                                                                                                                                                                                                                                               CCATCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCACAAGTA
                                             ACGTTCTCAT
                                                                                                                        ACCTTGAGAG
                                                                                                                                                                                                    ATTTAGATC
                                                                                                                                                                                                                                                                                                              TTTTTGCCAC
                                                                                                                                                                                                                                                                                                                                                            CAACGCGCGG
              ACGAGGAAGG
                                                                             TGGGCGACAG
                                                                                                                                         AGGAGTTCCT
                                                                                                                                                      TCTCCCGCTC
                                                                                                                                                                                                                                                                 GGGCCATCAA
                                                                                                                                                                                                                                                                                                                              TCAAGTATAT
                                                                                                                                                                                                                                                                                                                                             AACGCGGCTT
                                                                                                                                                                                                                                                                                                                                                                                          AAGAAGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGGTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAAGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTGAGAGC
                              TCTCGACGGA
                                                                                           TAAGACGGAC
                                                                                                          GTCAGCCGAA
                                                                                                                                                                      GGAATGAGCT
                                                                                                                                                                                      ATGAAGGAGG
                                                                                                                                                                                                                                                   AGAAGAAGAT
                                                                                                                                                                                                                                                                                GGTACTGCAA
                                                                                                                                                                                                                                                                                                                                                                            CGAGGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                           AGCAGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACAGGTTG
GACATTGAAA
              AGCTACGCCG
                                                                                                                                                      CTCTGGGACG
                                                                                                                                                                                    CGGCAGAGCT
                                                                                                                                                                                                    GTGTACCTAG
                                                                                                                                                                                                                                  TTCTGCAAGG
                                                                                                                                                                                                                                                  CAGAAGATAA
                                                                                                                                                                                                                                                                                                                                            GGCTTCTACA
                                                                                                                                                                                                                                                                                                                                                                                          AGGATAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACCCGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGAGAGAA
                              GTTGACGTCG
                                            AAAGACCCGG
                                                            AAGCGCTGTG
                                                                            ATTCAGAGGA
                                                                                                          GCCGTCTTCG
                                                                                                                        ACCGGCGAGA
                                                                                                                                         GAGCTTGGGA
                                                                                                                                                                      GCCTATGAGA
                                                                                                                                                                                                                                                                 TACAGGCAGA
                                                                                                                                                                                                                                                                               AGGCGCGCT
                                                                                                                                                                                                                                                                                                ATAACGATGA
                                                                                                                                                                                                                                                                                                               ACCGACGGAT
                                                                                                                                                                                                                                                                                                                                                            GGCAAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                           GTGATCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGTTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                        TACATCGTGC
                                                                                            TATCCTGTGA
                                                                                                                                                                                                                                                                                                                              ATGGAGTTCC
                                                                                                                                                                                                                                                                                                                                                                            GAGACGCAGG
```

FIGURE 17GG

(PCNA) - Vent DNA POLYMERASE FUSION PROTEIN

// Nucleotide sequence (SEQ ID NO: 35) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93E MUTANT: XXX = GAA,

486 162 216 270 324 378 432 540 594 648 SSS AAC ATA ACA SGA GCT AAT ACT GCA GAA AGA TTA GAA CTA CIC GCA CIC GAT AGC GAT GTT ACC TAC gcc GAT AAT GGA GAC AAA AGG AAG AAG ACT GAC ggg ACA GAG CAA GAA CIA GGA AAG TAT ATT GAG ATA GIT CTA GGA ggg ACA ACA AAG CAA ATT GAA GAC GAA GAG TTT GLL ATT GCA GAA GTT ATT ATG $_{
m LLL}$ GAG CTT ATG GTT GAA AAA GAG CAA CIGACA GAG AAA GAA CAA GGA AGA AAA GGA SGA AAA ATA GGT GIC ATA CAG AAA GAA GAA GIT GAG gad GLLGLI GTTAGA GTA AGC GAG GCT GTT ACC GGT AAG ပ္သင္ဟ GLL AGA TTA GAT GAC GAA ATC ATG ATG GTA CIA GAG GAC GAC GAA GAA AGT GAA ATA AGT GGA GII CTA AAT GAT TAT AAC AAG GIG GAG TCC CCA AAG ATC GAA GGA GAT AAA GCA gg GCA CIA ACA AGC AAG AAG CLL ATC ATG GAG ACT TCI GGA TAT TTT GTT AAG AAG GAA ပ္ပပ္ပ TTTCTA TTC GAG AGC AGA AGA GCC ATG GGA ATA GTC GGA AGT AGG ATA ATA CAC AAA CCA GAT AGC GAC AAG SG GCA ATG ACA CLL AAA $_{
m LLL}$ GAA GGA ACA GAA GTTTAT GLL TCA ATG CTC AGA GAA GAA AGC CTT GAT ACC

240 360 540 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG GGGCAAAATA TATATATGCT GAGACATGGA AAGGGAAGTT GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT CAAGCGTTAT TGTTAAAGAA AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA CCTTGCCTTT AATAATGATT GTATCTCATA GTCAGGAAAA AATTTTGGG CAGCTATGCG ATAAAGCGTT TTGTTCAAGT TTCAGCCCTA GAATTTGGAA AGGGCGAGAT TAAAGGGCGA TACCCTTTGC GGAGACGAGG AGCTTAAGCT GGGGACAATT TTGATTTGCC TATTGAGGAG ATAAAGGCAA CAAGACXXXC GAATATGACA GACCCTCATT AAGAGAAATG TGCAGTGAAA TCCCATGGAG TGAGGGAGAT AATAGAACTT CGAGCATCCC TGACATTTAC AACTTACAAT ATGACTCCGC GAGTGCTCGA TGTCCAATGA AGGCTTGAT ATGTGATAAT GGGAGTTTAA AGCTCATTTT CAGCTGTGGT CGTTTTATCA ATGAAGAAGA AAACGGGCAG CTTCTCAAAG AGTTATGCCG AAAGAGAACG GAAGTCTGGA GTCGATGTTG AAAGACCCCG AAAACTGTGA AGGGAACATC CTCATAGACA GATATTGAAA

1380 1500 1560 1740 1860 1920 1020 1200 1260 1320 1440 1980 2100 2160 1080 1140 1620 1680 1800 2040 2220 840 GCTGATAGGT GTATCTTTTA AGAGTATAAA AGGTTTGTGG TACTCACAAC TCCGATAGTA GGACTTAATT CGAAAAGAAA CGGCTATATG TAAGGTTCTT ACTCATTAAA GCTTGAGCTT TGCAGTCATA TTGGAGTGAG AAGTGTTGAA GGTTCCACTT AGCCATTGGC ACCGGGCACA AATCCACTTT TGAGGCAGTT TGCCGCTATA TGCTAGGGCA CGCATGGGGG AATTTTACTT TTTAAGGTAT AAACCAAGTT TCAAGGGTAG CTGATGAGGA AGCCAGAAAA ACGATGTTGC AAAAGCCTGA TAAGGAGAGA GAAAGGAGGA CGTATACGCT CAGAGGAAAT AGCTGGCAAA CCATACTCGG ACAGCTATTA AGTICGGCTT TTCCAGGTCT TTTGTTACAA AAAAGCGCTA TAAAAGTGAA GCGATAGGGT ACTACATAGA CAATGGAAGA TCGTGGAGTG CAATAATAGT TTGACCCGAT AAAGCGTTAC TTAAAGAGGG CAAAATACAG AGGACTACAA TGGCTCAAGA GGTAG 2325 ATAGAGGAAA GCTGTGGAAA CAGTIGIGG AAGGACGAIA AACCICCCAA GAGATCAAGC ACCGGCAACC AAATCCACAA TTGCTTGCAA ATACCCGGGG AACTCCAAAC TTGGAAGTAG GAGGCTATAC GAGAAAATAG GGAAAGATAA GATCCGGACT TTTGGATACA ATTCTTCCCC ATGGAAGCTG TATGTAAAAG TGTAAGAATT GAATGTGCTG AGGGATTTAA GCAAGAGGGA AAATTAGGAG CTGTACCCTT TTTATTCCCT GCCCAGTACT CCGAACAAAC TTATGCCACA TGATAGTTTT CTTTCCGGGC GATAAGAGAA GAGAGGATTC GCAGGATAAC AACAAGGGGC GCAGATTACC CTTAGATGCA AACCAAAAGC TGAACTTGCA CCTGGGAGGA AAAAGAGGGC GAAGAAAATG GGCTATTAAA AAACTACATA AAAGGTTTTA CAAAGGGAGC ATCCTAGAAA ACACAAGTAC ACTCGAAGCG GAAAAAACTA TTTCCGCAGT GTACTCGAAG AGATGTTGTA AAGACTTGCC ATACCCTTGA TACTTAGGAT AACAAACCGG AGAGGATGGG TTTTAGGAAA AAGAAAGCAT TCGGGAAGGA ACGCGAGGAA GAACAACTTA TCTGCAAGGA ATAGGCAAAG GCTTTTACTT AGACTCAGGC AAGTTGTTAG CGATAGCAAA GGGACGTCTC TTTATTTGGA AGGCAAGATG TAGAGATGAC CTGACGGCTT ATATCGTTCT AAGATATAAA AGGAATTCCT TTATCCATGA CCCAAGATTC ACGTATGAGC ACAGAATACG CAAAGCTCAA TGGGAAACAG GTATCCCCAG TATGCGGACA ATAGCTAAGG CCTCATGTCG ATAATAAGCT GATCTTTCC TATGAAGCAG AGGGTGGCAT CGGCGCTTAA GAAAATATCA GGATATAGGT GCAATGAGGC AGACACTACA GAGTATGAGG GATGAAGAGG AAAGCTGTAG TTGCCGGCAG CAAAGTGTAT AAGAAAGCCA GAAAAGCTTG ATGCTCGATT GGGTATCCTA

Figure 17HH

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 67) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

1020 1500 1080 1200 1260 1380 1440 1560 1620 1140 1320 1680 360 540 600 9 840 900 960 TGCAGTCATA CTATAATCCG AATTTTTAAG TATATATGCT GAGACATGGA AAGGGAAGTT GGCCAAAATA CAAGCGTTAT CCTTGCCTTT TTTGCCGTAT GTATCTCATA ACATCCCGAA AATCCACTTT TGAGGCAGTT TGCCGCTATA TGCTAGGGCA GCTGATAGGT GTATCTTTA AGAGTATAAA AGGITIGIGG TCCGATAGIA GGACTTAATT CGAAAAGAAA CGGCTATATG CGCATGGGGG TAAGGTTCTT ACTCATTAAA GCTTGAGCTT AATAATGATT TGTTAAAGAA TACTCACAAC GAGAGGATTC TTTGTTACAA AAAAGCGCTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG CTGATGAGGA TTCAGCCCTA TAAAGGGCGA GGGACAAAGA TCAAGGGTAG CAGAGGAAAT CAATGGAAGA TCGTGGAGTG ACGATGTTGC ACAGCTATTA CAGCTATGCG TACCCTTTGC AGCTTAAGCT AGGCCGAGAT AAAATATCGA CGTATACGCT AGCTGGCAAA AGCCAGAAAA TTGACCCGAT AAAGCGTTAC AAAAGCCTGA TIGITCAAGT TTGATTTGCC CAATAATAGT CCATACTCGG AGTTCGGCTT AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GGAGACGAGG CATAACAAA GATGGCAAGC TATTGAGGAG ATAAAGGCAA CAAGACXXXC GAATATGACA GAATTTGGAA GGCCAGAGTA ATCACATGGA AAGAGAATG ATAAAGCGTT GTCTTAGGAA GCTGTGGAAA CAGTIGIGG AAGGACGAIA AACCICCCAA ATGGAAGCTG ACCGGCAACC CCGAACAAAC TATGTAAAAG TGTAAGAATT GAAGAAATG AAATCCACAA TTGCTTGCAA GATAAGAGAA ATAGAGGAAA TTATGCCACA ATACCCGGGG GACCCTCATT GGGGACAATT TTTTAGGAAA AACCAAAAGC AAATTAGGAG GCCCAGTACT GAATGTGCTG CTGTACCCTT TITATICCCT ATTCTTCCCC CGAGCATCCC TGAGGGAGAT AGTTCGGCTT GAAAAAACTA GAGATCAAGC CCTGGGAGGA GGCTATTAAA GTACTCGAAG AATAGAACTT TGACATTTAC TCCCATGGAG AACTTACAAT TGATAGTTTT TGAACTTGCA TTTCCGCAGT AAAAGAGGC CTTTCCGGGC ATGATACTGG ACACTGATTA GGGAGTTTAA TGTCCAATGA AAAAGCTGGG AGAGGATGGG ATACCCTTGA ATGACTCCGC CAGCTGTGGT AGGGCTTGAT ATGAAGAAGA ATGTGATAAT AAGAAAGCAT TCGGGAAGGA GGGACGTCTC ACGCGAGGAA AAGATATAAA ATAGGCAAAG GCTTTTACTT AGCTCATTTT CGTTTTATCA GAACAACTTA TTTATTTGGA TCTGCAAGGA AGGCAAGATG TAGAGATGAC CTGACGGCTT AAAGAGAACG CTTCTCAAAG AAAACTGTGA GAAGTCTGGA AGGGAACATC CTCATAGACA AGTTATGCCG GTCGATGTTG AAAGACCCCG AAACGGGCAG CCCAAGATTC CAAAGTGTAT GAAAATATCA GTATCCCCAG AAGAAAGCCA GAGTATGAGG TATGAAGCAG ACGTATGAGC AGGGTGGCAT AGACACTACA TATGCGGACA GATATTGAAA **FGGGAAACAG** CGGCGCTTAA ATGCTCGATT GGGTATCCTA GATCTTTCC GGATATAGGT GCAATGAGGC

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1920
                               1980
                                              2040
                                                              2100
                                                                             2160
                                                                                             2220
                                                                                                              2280
TAAGGAGAGA TTGGAGTGAG
              AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA
                               GGTTCCACTT
                                                AGCCATTGGC
                                                               TAAAAGTGAA ACCGGGCACA
                                                                             GCGATAGGGT AATTTTACTT
                                                                                            AAACCAAGTT
                                                                                                              TTTAAGGTAT
                              CAAAATACAG
                                             AGGACTACAA
                                                                                             ACTACATAGA
                                                                                                              GAAAGGAGGA
                                                                                                                             GG 2325 //
                                                                             GGAAAGATAA
                                                                                             GATCCGGACT
 TTGGAAGTAG
                               GAGAAAATAG
                                             AGGGATTTAA
                                                               GCAAGAGGGA
                                                                                                            ITGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA
                                                                                                                            CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA
 GCAGGATAAC AACAAGGGGC
                               AGATGTTGTA
                                             GCAGATTACC
                                                             AAGACTTGCC
                                                                             CAAAGGGAGC
                                                                                            ATCCTAGAAA ACACAAGTAC
              AGACTCAGGC
                                                            CGATAGCAAA
                                AAGTTGTTAG
                                              TTATCCATGA
                                                                             ATATCGTTCT
 GATGAAGAGG
              ATAGCTAAGG
                              AAAGCTGTAG
                                                                             ATAATAAGCT
                                                                                            ACAGAATACG
                                             GAAAAGCTTG
                                                              CCTCATGTCG
```

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540
             216
                  270
                       324
                           378
                               432
                                    486
                                             594
                                                  648
         162
                                                       702
         CCG
                  ATA
                       ACA
                                     AAT
                           CCA
GCT
                                         ACT
                                             GCA
             GTT
                  TTA
                       GCA
                                     GAA
                                         CTA
                           CTC
         CTC
                               GAT
                                             AGC
                                                   GAT
                                                       ATT
     GAT
                  ACC
                                     AGG
                                         AAG
                                              AAG
                                                       TAC
                       ACT
                           GAC
                                AAA
                                                   ggg
              GGA
                                     GCC
                       GGA
              ATT
                  GAC
                                CTA
                                         ATA
                                              ACA
     GAA
                           GTT
                                                       TAT
                                                   AAG
     ACA
                                         GAG
                                             GAG
              ACA
                   AAG
                        CAA
                           GAA
                                GIC
                                    ATT
                                                   GGA
TTT
     GTT
              GAA
                  GCA
                                     TTT
                                              GAG
         ATT
                           ATG
                                                   CTT
                       ATT
                                 GAA
                                         GTT
                       ACA
     AAA
                           GAG
                                                       CAA
         CIG
                                     AAA
                                         GAA
                                              GA
                   AAA
                                                            AGA
              CCA
                                GGA
                                                   GGA
                       ATA
                   GGT
                                     ATA
              GAA
                           GAA
                                         CAG
                                CTT
GCA
    gag
              GTT
                       GAG
         GTT
                   AGA
                           GTA
                                GTT
                                     AGC
                                             GAG
                                                  GIT
                                         ACC
    ggg
                                     GAC
                                                       ATG
GGT
         AGA
              GTT
                   AAG
                                                  ATG
                        TTA
                           GAT
                                GIA
                                         GAA
                                             ATC
                   CIA
GAA
    GAG
         AGT
              GAA
                       TIC
                           ATA
                                GTT
                                    AGT
                                         GGA
                                              GAC
                                                   GAC
                                                       GAA
    GAT
         CCA
             TAT
                       AAC
                                AAG
                                    GTG
                                             TIG
                                                   JCC
                  ATC
                                         GAG
    ATA
         GAT
              AAA
                   AAG
                       GAA
                                    CTA
                                         GCA
                                             TTA
                                                  GIG
                           gg
                                GCA
ATC
         ATG
             AGC
                  AAG
                       GAG
                                         AAG
                                             GGA
                                                  TAT
                                ACT
                                                       TTT
                                                            CTT
                                    TCT
                           GTT
             _{
m TTT}
    AAG
                                                  AGC
                                                       AAG
         ggg
                   CIA
                       GGA
                                TIC
                                    ggg
                                         ATG
                                             GAG
                           AGA
                                                       ATA
    AGT
             ATA
         AGG
                  CAC
                       AAA
                            TTT
                                CCA
                                    GAT
                                         ATA
                                             GAT
                                                  GIC
         ATG
             AGC
                       AAG
                                     AAA
CCA
    GCA
                                CTT
                                             GAA
                                                  GGA
                                                       ACA
                           ACA
                                         TTT
                  GAC
                                                            GAA
             TCA
                  ATG
                      CTC
                                    GTT
                                                  TAT
         AGC
                           AGA
                               GAA
                                         GAA
                                             CTT
                                                       GTT
```

Figure 17II

Deep Vent- (PCNA) DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 67)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 240 300 360 420 480 540 600 999 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380 1440 1560 1620 1500 1680 1740 1800 CGATTATAAG GATTTTCAAG TTAGACCTTA CATTTACGCT GAGGCATGGG GAGGCCGATT GGATAAGATA GAAGAGGTAC TATAATGATA TCTCCCGTAC GATAAGGGAG TGAGCCAAAG CTTTGACCTC AGTTTATGAG GGCCTGGGAG GGTAACGTAC CCTCAGGAAG TAACGICICA ATTGGATGAA TTATGGGTAC GGGGAGGGAA CTTATACATA AAAGAAGAAA GCTTGAGTAC GATAGATGAG CGAAATAGCC GCTCGCATTT CTATCTAGTT CGGCCAGCCC CGAGAGAAGG CTGGGAGGGG GGTTGGGCAC GAAGATGCTT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) GGGGCTTGAA ATAGTCAGGA GGGACTGGAG TAATCACCCA TAACCGCCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT AAGGAGCCGG AGAAAGGGCT GCAAACAGCT ATTATGGGTA AGTTCCTGGG CCGCAATAAG TTCCGTTCGC AGGGGCCCAT AAAAGATCGA TCGACCTTCC GGGACGGTAG GAAGGATACA CCCTCGAGGC AGATAGCTGA AGGATGCAAA CAAGGTTAGT AGTGGTACCT AAGCCGGATG AGAGGGAGTA TCGCCCCAGA TCAAGAGGTT TTACGGCCTG GGTTCAAAGT CCGAGGAGAT GTTCTTCGTG ACGAAGAGA AGTATGCGTT GGCGATGAAG AGCTCAAGTT GGCTGTTGGA CAATCGAGAA ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC AAAGAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT GTTAGGAAGA GAGTACGACA GAGTTCGCGA GGCGATTCTT TACGCTCACG TATTCAATGG AACTTGGTGG CCCTCGATAA CCCAGCCTGC TCTAAAGACC GAAAGTTCG GGGCAAAAC TATAAACGCC AAGCTCCCAG GTAAGGAAGA CAGGACXXXC ATAACGTGGA CCCCTGGGAA GAATACGATG GCAGAGAGCG V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, GAGATAAAGG CCAACATACA GCCCAGCTTT GGCTCCAAAC GGGATACGTT CICCICAAAG AIGACICGCA GAIIGAIGAG GGCTGTACTT TGAACACCCT TCCAATGGAA AGCCAAAGTC TTCAACTGGC TGCCGAAAAG CCGCAGTTAT TGACATCTTT CGAAGGGGAG GATAAACCTC GGAGAAAGTT AGTTGCAAAG GATGAAAGCT TACCTACAAC GATAAAGCTA GACAGCGGTG CCCAATGGAG GAGCCTGTAC GGGGTTTATC CAAAATCCTG TAAGGAGTGC GGAACTGGAG CACAATTCCT AGGGTGTAGG GACTGGAGAG GAAGGGAAGA TAATCACTAG GAATTATAGA AAGGCCTAAT GCTACGCTGG TAGATTTCAG ACGTGAGAGG ATGAGGAAGA TTTCCAGCGA ATGTTATAAT AAAAGCTCGG TTGGGGATAT TTAGGAGAAC GAAAGCCAAA GGGAGTTCTT TTTCTAGGTC GGAATGAATT TGAACAGGGA AACGGGCAAT GTTGGTACTG GACTCTACGC TCGTAGATTA CCCTCTATCA AGGACTTCCC TAAAAAGGAA TCGTAAGGAA CTAATAGACA GTCGAGGTAG AAAGATCCCG ACTGGAAAGG GATTACAGGC AAGATAGTGA GAGGTATGGA GACATAGAAA AGCTATGCTG AAGAGGCCG GCAATCTTCG GCCTACGAGA TTAGTTTCCC GCCCTAGAGT AGAGAGCATT ATGCAGAGGC TACCACGTGA GAGCTCGGTA CTGTGGGATG CTAAGGGAGA CCGGATACGC AAGTTCTGCA AGGCAAGAAA GCAAAAGCCC TATATAGAGT GACACAGATG GAGGCCTTCT

		54	108	162	216	270	324	378	432	486	540	594	648	702	
1920 1980 2040 2100 2160	2280 2328	GAC	ATA	CCG							ACT		GAA	AGA	
		ATA	ggg	CIC	GTT	TTA	GCA	CIC	GAT	GAA	CTA	AGC	GAT	ATT	
ABGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	AGA	CTT	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ggg	TAC	TGA
TGAGGAGGCA TCCAGAAAG AGGTCCGCAC CATGGTGATA TGCAGAGGAG	GTGGCAGAAG	CAA	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ggg	ATA	ACA	AAG	TAT	GAG
		ggg	ACA	GAC	ACA	AAG	CAA	GAA	GTC	ATT	GAG	GAG	GGA	GAG	GAA
ATGGCAACGT ACGAAATACC ACAAGGCTAT TGAGGCCTGG GGGCTATCCT	CCTC G //	$\mathbf{T}\mathbf{T}\mathbf{I}$	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TTT	GTT	GAG	CTT	ATG	GTT
ATGGCAACGT ACGAAATACC ACAAGGCTAT TGAGGCCTGG GGGCTATCCT	AAGACCTCAG AGAAG //	GAG	AAA	CIG	CCA		ACA				GAA	CAA	GGA	CAA	AGA
		AAA	TTT	GIC	GAA		ATA		CTT			GII		ATG	CC.
ATCCTAAAGC CTGAGCAAGT CTTCACGAGT GGAGTAAAGG ATAAGCAAGA	TACAGGAAAG AACATCAAGA	GCA	ggg	GLT	GLT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	ပ္သပ္သ	GCT
		GGT	ပ္ပင္ပ	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
CCTAGAGGCT AACTGAAAAG CACGAGGCCC AGCCGCTAGA AGACGGCCCA	GGCCTTTGGG	GAA	GAG	AGT	GAA						GGA	GAC	GAC	GAA	CTA
TAGA CTGA CGAG CCGC ACGG	CCTT	TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TIG	IGG	AAT	TIC
. , , -		GTA	ATA	GAT	AAA	AAG	GAA	ပ္သ	GCA		GCA	TTA	CIC	GGA	ACA
AAAG GAGG CAGA AGGT AGGG	TTAG	ATC	TTA	ATG	AGC				ACT			GGA		TTI	CTT
AAGCAAAAGT TTAAGGAGGT ACGAGCAGAT CAAAAAGGTT TGCTGAGGGG	GAATATTAGA CAGGTCTTAC	GAA	AAG		TII				TIC			GAG	AGC	AAG .	AGA
		TII	AGT	AGG (ATA '	CAC			CCA			GAT (GIC	ATA	GGA
AAAC AGAT, ITAT' CCGT' ACAT,	TTCT	CCA	GCA 7	•	AGC 7			ACA .		AAA (•	GAA (GGA (ACA 1	GAA (
AAAGAAACCC GTAAAGATAG CTAGTTATTT GTTGCCGTGG GGGTACATAG	GCCGTTCTTA	ATG (ACC (TCA 7	_		AGA 1	GAA (_	TAT (GTT 1	GAT (

Figure 17JJ

(PCNA) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38)

FIGURE 17JJ (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	216	270	324	378	432	486	540	594	648	702	
GAC	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
ATA	GGG	CIC	GTT	TTA	GCA	CIC	GAT	GAA	CTA	AGC	GAT	ATT	
CTT	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ggg	TAC	:
CAA	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ggg	ATA	ACA	AAG	TAT	GAG
ggg	ACA	GAC	ACA	AAG	CAA	GAA	GTC	ATT	GAG	GAG	GGA	GAG	GAA
TTT	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TTT	GTT	GAG	CTT	ATG	GTT
GAG	AAA	CTG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
AAA	TTT	GIC	GAA	GGT	ATA	GAA	CTT	ATA	CAG	GTT	AAA	ATG	CCA
GCA	ggg	GLL	GTT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	င္ပင္ပ	GCT
GGT	ပ္သင္ပ	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
GAA	GAG	AGT	GAA	CTA	TIC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TIG	TCC	AAT	TIC
GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CIC	GGA	ACA
ATC	TTA	ATG	AGC	AAG	GAG	GTT	ACT	TCT	AAG	GGA	TAT	TTT	CLT
GAA	AAG	ggg	\mathtt{TTT}	CTA	GGA	AGA	TIC	ggg	ATG	GAG	AGC	AAG	AGA
TTT	AGT	AGG	ATA	CAC	AAA	\mathtt{TTT}	CCA	GAT	ATA	GAT	GTC	ATA	GGA
CCA	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	$\mathtt{T}\mathtt{T}\mathtt{T}$	GAA	GGA	ACA	GAA
ATG	ACC	AGC	TCA	ATG	CTC	AGA	GAA	\mathtt{GTL}	GAA	CTT	TAT	GTT	GAT

9	120	180	240	300	360	420	480	540	900	099	720	780	840	900	960	1020
GATTTTCAAG	TTAGACCTTA CATTTACGCT	GAGGCATGGG	GAGGCCGATT	GGATAAGATA	GAAGAGGTAC	GCTCGCATTT	TATAATGATA	TCTCCCGTAC	GATAAGGGAG	CTATCTAGTT	TGAGCCAAAG	CTTTGACCTC	AGTTTATGAG	GGCCTGGGAG	GGTAACGTAC	CGGCCAGCCC
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG	TTAGACCTTA	GITAGGAAGA TAACCGCCGA GAGGCATGGG	AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT	TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA	TGACATCTIT GAGTACGACA TTCCGTTCGC GAAGAGGTAC	TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT	CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT	ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC	TITCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG	ATGITATAAT TACCTACAAC GGCGAITCIT TCGACCTICC CTAICTAGII	AAGAGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	TIGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC	CCAACATACA CCCTCGAGGC AGTTTATGAG	TACGCTCACG AGATAGCTGA GGCCTGGGAG	TATTCAATGG AGGATGCAAA GGTAACGTAC	GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC
GATGGGAAGC	GACAGAAACT	GTTAGGAAGA	GTAAGGAAGA	CAGGACXXXC	GAGTACGACA	GGCGATGAAG	GAGTTCGCGA	ATAACGTGGA	ATAAAGCGGT	GGCGATICTT	CCCCTGGGAA	GAGATAAAGG		TACGCTCACG		GCCCAGCTTT
CATCACCGAG	GGTTGAGTAC	GATTGATGAG	TGCCGAAAAG	TGAACACCCT		TCCAATGGAA	CGAAGGGGAG	AGCCAAAGTC	GAGGGAGATG	TACCTACAAC	GATAAAGCTA	GACAGCGGTG	TTAGGAGAAC GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG
ACGCTGACTA	AAAGAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT	CTCCTCAAAG ATGACTCGCA GATTGATGAG	GAATTATAGA	GAGGTATGGA GGCTGTACTT	AGAGAGCATT CCGCAGTTAT	CTAATAGACA AAGGCCTAAT	GACATAGAAA CCCTCTATCA	ATGAGGAAGA		ATGTTATAAT	AAAAGCTCGG	TTGGGGATAT	TTAGGAGAAC	GAAAGCCAAA GGAGAAAGTT	ACTGGAAAGG GACTGGAGAG AGTTGCAAAG	GGGAGTTCTT
ATGATACTTG	AAAGAAAACG	CTCCTCAAAG	AAGATAGTGA	GAGGTATGGA	AGAGAGCATT	CTAATAGACA	GACATAGAAA	AGCTATGCTG	GTCGAGGTAG	AAAGATCCCG	AAGAGGGCCG	ATGCAGAGGC	TACCACGTGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA

REPLACEMENT SHEET

FIGURE 17JJ (CONT.)

CIGIGGGAIG	TITCIAGGIC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
SCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CIPAGGGAGA	GCIACGCIGG	GGGATACGIT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
ITAGITICCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGICICA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
SATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
SCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
IATATAGAGT	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
SACACAGATG	GACTCTACGC	CACAATTCCT	GGGCCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
SCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
SAGGGCTTCT	ACGTGAGAGG	GTICTICGIG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
SAAGGGAAGA	TAATCACTAG	GGGCCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
STAAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
STIGCCGIGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
3GGTACATAG	TGCTGAGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
ITCGAICICA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGITITACCI	2220
SCCGTICTIA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17KK

JDF-3 - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 67)

FIGURE 17KK (CONT.)

CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

ttcgccaagcgctacctcatagacaagggcctaatcccgatggaaggtgaggaagacttaaactcatgtcgtdgadatcgadacgctctaccacgagggagaagagtttggaa acgecegtegetacetacateaaggagceggagcaggacagatatcetagactatactagactttcetagtctctadcetatcaatcataatcacccacaacgtctcgccagatac CAGGICIGIGGAGGICTGGGICCICIACIICACGCACCCGCAGGACXXXCCGGCAAICCGCGACAAAIAAGGAAGCACCCCGCGGGICAICGACAICIACGAGIACGACAIACCC **ACCCTCGGGAGGGACGCGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTTCGACCTTTATCCAGTCATAAGGCGCACCATAA** ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCCGGCGAGGGGGCTTGAGAG CAGAAGATAAAGAGGAAGATGAAGCCAACTCTCGACCCGCTGGAGAAGTCTCCTCGATTACAGGCAACGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGC actggagcgagatagcgaaggagagaggcgaggggttttggaggcgatactcaggcacggtgacgttgaagaggccgtcagaaattgtcagggaagtcacccaaaaagctg GITAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGGTTCGACCCGACGAAGCACAAGTACGATG CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCCG GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACGACGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGAGCTTT GGTCGCGCCTACTCGATGGAGGCGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATGTAATCCAAACTGCCGGCCTTCTC GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGGGTTTGGCCGACGAGGT ATGATCCTTGACGTTGATTACATCACCGGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAAGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

54	108	162	216	270	324	378	432	486	540	594	648
GAC	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA
ATA	999	CIC	GII	TTA	GCA	CTC	GAT	GAA	CTA	AGC	GAT
CTT	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ggg
CAA	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ggg	ATA	ACA	AAG
ggg	ACA	GAC	ACA	AAG	CAA	GAA	GIC	ATT	GAG	GAG	GGA
$_{ m TTT}$	GTT	ATT	GAA	GCA	ATT	ATG	GAA	$_{ m LLL}$	GLT	GAG	CTT
GAG	AAA	CTG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA
AAA	TTT	GIC	GAA	GGT	ATA	GAA	CLI	ATA	CAG	GTT	AAA
GCA	ggg	GLT	GLT	AGA	GAG	GTA	GIT	AGC	ACC	GAG	GLI
GGT	ggg	AGA	GIT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG
GAA	GAG	AGT	GAA	CTA	TIC	ATA	GIT	AGT	GGA	GAC	GAC
TTT	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TIG	ICC
GTA	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CIC
ATC	TTA	ATG	AGC	AAG	GAG	GIT	ACT	$\mathbf{I}^{\mathbf{C}\mathbf{I}}$	AAG	GGA	TAT
GAA	AAG	ပ္ပင္ပ	TTT	CTA	GGA	AGA	TIC	ပ္ပင္ပ	ATG	GAG	AGC
TTT	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GIC
CCA	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	TTT	GAA	GGA
ATG	ACC	AGC	TCA	ATG	CIC	AGA	GAA	GLI	GAA	CTT	TAT

FIGURE 17KK (CONT.)

702 CCC ATG CAA ATG GAG TAT TAC ATT AGA GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA GGA AAT GAA ATG TTTAAG GIT ACA AIA

Figure 17LL

(PCNA) - JDF-3 fusion protein

// Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 39) Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 67) CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, V93E MUTANT: XXX = GAA,

162 216 270 324 378 432 486 540 594 648 702 CCG ATA ACA CCA AAT ACT GCA GAA ATA GGG CIC GTT TTA GCA CTC GAA CTA GAT ATT AGC TAT TAC AAT GGA GAC AAA AAG AAG ပ္သင္ဟ GAT ACC AGG ACT CTA ATA CTA GTT GAC GGA ပ္သင္ဟ ACA AAG GAA ATT ACA ; GAG ACA GAC AAG GAG GAG GGA GAA CAA GAA GTC ATT GTT ATT GAA GCA GTT CTT ATG ATG GAA $_{
m LLL}$ GAG GTT ATT CAA AAA AGA AAA CTG CCA AAA ACA GAG GGA GAA CAA GGA GIC CCA GGT CTTATA GAA CAG GTT AAA ATG ATA GAA S GTT ggg GTT AGA GAG GTT AGC GII GCT GIA ACC GAG gcc AAG GTA GAA ATG ATG AGA GAT GAC ATC GTT GGA CIA AGT GAA CIA GAC GAA GAG GTT GAC TIC ATA AGT CCA TCC AAT GAT TAT AAG GIG GAG TIG AAC AAG ATC ATA GAT AAA GCA GCA GGA GAA CCC CIA TTA ACA AAG CTT ATC ATG AGC GAG ACT AAG GGA TAT TTTGTT TCT ggg TTT CIA TIC ATG AAG AGA AGA gcc GAG AGC GGA ATA ATA AGT CCA GIC ATA CAC AAA TII GAT GAT AGC GCA ATG GAC AAG ACA CTT AAA TTT GAA GGA ACA GAA AGC TCA ATG GAA GLT GAA TAT GTT CIC AGA CTT ACC GAT

CTACTICTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGGAGAAGGTGA ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCC AGAAAAGTTCCTCGGCAGGTCTGTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATC

FIGURE 17LL (CONT.)

agcegegactetegegacaatatcetetatctagactttcetagtctctaq<mark>cct</mark>tcaatcataatcaceceacaacetctceccagatacectcaaccecaagegegetet GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATG GCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGAGGAGGAGGGCAAGATAACCACGCGCG GCACGTAGCCATAGCGAAGGGTTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGG CGATTCCCTTCGACGAGGACCACGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGC CAAGGTGAAGGGCAGGGTACACTTTCGACCTTTATCCAGTCATAAGGCGCACCATAAAACCTTCCCGACCTACACCTTTGAGGCTGTATACGAGCGGTTTTTCGGCAAGC CCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAG CTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCCCGGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCT CCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGGAGGTTGAGGAAAAGTTCGGTTTTAAA GTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACT GCTTGAGATAGTCAGGCGCGCGACTGGAGCGAATAGCGAAGGACGCAGGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAATT GTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCC CTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAACATACGGCGACAAACTTC TACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Figure 17MM

Sac7d gene (ACCESSION No: M87569)

Nucleotide sequence (SEQ ID NO: 69) Amino acid sequence (SEQ ID NO: 70)

36 67 54 162 M V K V K F K Y K G E E K E V D T S ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAA AAA GAA GTA GAC ACT TCA GAC N G K T G R G A V S E K D A P K E L AAT GGT AAG GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA K I K K V W R V G K M V S F T Y D AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC > 团 × L D M L A R A E R E K K * TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG TAA 团 团 Ö × V K V

Figure 17NN

Sac7d-Taq DNA polymerase fusion protein

Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)

M V K V K F K Y K G E E K E V D T S ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAA GAA GTA GAC ACT TCA

DGAC K I K K V W R V G K M V S F T Y D AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC N G K T G R G A V S E K D A P K E L AAT GGT AAG GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

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I ATC AAC ACC ACG Y TAT IATC AGCC S AGT V 3TG PGG PGG I ATC E r CTC gcc Bcc RGG CTA D 3AC Y E GAG r Si o CAG M M ၁ ဗိုင္ဗ r CTG E CIT AAC ₽ CCC r CTG E GAG GCC CCC CIG W TGG T ACG R AGG ი მმმ AAC AAC TGG ₽ GCC A GCC F CTT V GTC R CGG CAC ဗ္ဗဗ္ဗ LCTT gcc E 3AG s AGC д ССС **₽** CTT EGAG V GTG ი მვვ ್ದರ Y TAC I ATC ACG ල වූ v GTG GAC E T GAG ACC E CAC CAG CIC မ ၁၉ CTC M ATG LCTA ₽ 225 **₹** ACC. r Tr CAC CTG R AGG E GAG ဗ္ဗဗ္ဗ s AGC r CTG DGAC ACG CGC CGC CTA s TCC H T CAC ACG S TCC A GCC DGAC **₽** V GTC TGG c TC A GCC ACC IATC P CCG K AAG F ည် CAC GAG r CTG L TTG r CTG s TCC r TTG T ACG ი წვ D I GAC ATC V E GTG GAG ი მმმ යි දි CIC R ည် CAG I ATC gcc gcc V GTC A GCC EGAG GAG TTC V GTC N AAC AAC A GCT R AGG K AAG DGAC E r CTG R AGG စ ဗ္ဗ IATC I ATT F CAG 4 ರಿ V GTG r GTT S r CTC v GTC R CGG Y TAC LCTT Y TAT GAG GAA CCC cic IATC ACC a വൂ R AGG ი მმც R AGG gcc gcc A GCC A A A B ACC N AAC GAG ი გვ က ည гCTG H ACC F CTC v GTG ₽ GCC ¥ ₹ R AGG E CAG E GAG gcc Gcc s AGC CAC r CCC CCC E CAG GAC k AAG DGAT E GAG CIC GAC ACG GAG r CTC R GGG I ATA F N AAC r CTG AAG CTG CAG V GTC V GTG G G G R r CGC R s TCC အင္လ GCC 3 s TCC ဗ္ဗဗ္ဗ CIC K AAG ဗ္ဗဋ္ဌ s AGC IATC EGAG GGC R A S s AGC

P Y ဗ္ဗဋ္ဌ EGAG AGCC A GCC V GTG ი წმ ACC ය විව o CAG r CTG CTA F უ ცვ E GAG E GAG L E A CTA GAG GCC F N M P V TTC AAC ATG CCC GTC R AGG K AAG E S AGC SGG GGG r CHC M M CCC A GCC V GTC V GTC CAG CAG R AGG R AGG F S TCC F TTT r CTG ₽ GCG GAG E G Y V P D TAC GTG CCA GAC r CTC e Gag R CGG L CTC K AAG Y TAC K AAG D GAC R င္ပင္ပင အင္လ GCC A GCC V GTG H MATG E GAG H CIG r CTG M ATG v GTC CTG A GCC MATG I ATT ය විව E K T GAG AAG ACC CCC CCC ස විව ය විව A GCT CAG gcc Gcc s TCG F GAC က္ဆင္လ CTG CTT M ATG GAG A GCC V GTG ය ප K AAG V GTG CAG A GCC CTC A GCC යියි gcc Bcc I ATT စ္မမ္မ A GCG M ATG Y TAC M ATG A GCC GAG L F CTC TTC (¥ DDI D L GAC CTC E GAG CTC GAG E GAG R AGG A GCG R GGG V GTC gcc Gcc CGG A GCC E R AGG T ACC GGG A GCC CCC CCC X IAC v GTG ပ ညီ უ წ E GAG V E GTG GAG K V AAG GTG s AGC A GCC V GTC F M ATG AAA PCCT ဗ္ဗဋ္ဌ NAAC I K AAG T ACC GAA CCA

™ TGG GAC GAG ggg ט I ATA V G GTG GGG E V GTG E CTG CCC V GTG ggg Ø L CCC TAT × V GTG

H H H ත ති ဗ ဗ္ဗ g GGA ဗ္ဗဗ္ဗ ဗ္ဗင္ဗ g GGC D GAT ı ATT ဗ္ဗဗ္ဗ GAG AAG A GCC s TCC r CTC

H H * CAT CAT TAA

Taq DNA polymerase-Sac7d fusion protein

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)

1/ GGC GGC GGT

V GTG ACC K AAG r CCC P CCA ය ශීශීශ CTG K AAA r CTC V T S G M L P L F E P K G R V L L GTC ACT ACT GG ATG CTC CTC TTT GAG CCC AAG GGC CGG GTC CTG CTG D G H H L A Y R T F H A L K G L T GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC A CCC T ACG $_{
m L}$ s AGC GG GAG CCG GTG CAG GCG TAC GGC TTC GCC AAG AGC CTC D A V I V V F D A K GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG Y G G Y K A G R A P TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC A L I K E L V D L GCC CTC ATC AAG GAG CTG GTG GAC CTC V L A GTC CTG GCC A K K A E K E G Y E V R I L T A GCC AAG AAG GCG GAA AAG GGG TAC GAG GTC CGC ATC CTC ACC GCC G Y E A D D
GGC TAC GAG GCG GAC GAC P CCG P R Q L CCC CGG CAA CTC ი გენ 4 325 v GTC H E L E CTC GAG (K E D AAG GAG GAC R CGC F TTT R S R AGC CGG (A L GCC CTC 1 S F TCC TTC E D GAG GAC L A CTG GCG

K AAG L CTG DGAC L LCTT ₽ GCC A 3CC A GCC r GTG ₩ IGG GAA V GTC I ATC T R AGG တ္မွင္မ g GGG A A V GTT LCTG r CTG CTC ი მმმ CAG K AAG D P M L GAC CCC ATG CTC ი მმმ S AGC R E F E GAA Y TAT s AGC E GAG DGAC CIT GAG P CCG V GTG E CCT CCC D GAT GCC CCC P CCC ი მ<u>ვ</u>მ R CGG r CTG W TGG G G G K AAG P CCG GAC CAC R AGG CAC A GCC E CIT DGAC GGC CTG E E GAG GAG A I GCC ATC к Адд V L GTC CTC A GCC ₩ TGG P CCC P L CTC CCC T G D E S D N ACC GGG GAC GAG TCC GAC AAC G D GGC GAC C CTG M ATG A GCC e Gag r CTC W TGG A GCC L L CTT CTG (CTC Y GC PP s AGC R CGG D GAC R CGG P CCC က် သည် S D R I H TCC GAC CGC ATC CAC W E K TGG GAA AAG K AAG (g GGC TGG r Agg gcc GAG CAC L GCC CCC A K GCC AAA F PCCG E K T A R K GAG AAG ACG GCG AGG AAG r CTG s TCC E GAG AAG V GTC ი მვც R CGG CIC CGG CTC E GGC ස ප E CTT L D CTG GAC ဗ ဗ္ဗ A GCG K AAG F r CTT r CTG s TCC ი მმე CTT CTG CTG GAC R AGG r CTT ი მმ E CIT P A W CCG GCC TGG A GCC Q L CAG CTC (L K CTG AAG E G GAA GGC ₽ GCC N AAC ۷ GTG GAG K AAG R AGG D GAT v GTG L CTG S S S S S S AAG A GCC E GAG GCC CCC F TTT GAC L R CTG AGG D L Y GAC CTT TAC CTC Y ი მვვ r CTG GAC L I T CTC ATC ACC M ATG F TTT ი მმე GCC GCC s AGC L R CTC AGG GAC I ATC L CAC P CCC GAA v GTG A GCC A GCC A GCC ဗ္ဗဋ္ဌ L CTG F CTG A GCC gcc gcc L R AGG

ACC IATC N AAC I A T ACG F မှ ပို့ V GTG S AGT E CIC E A GCC CTC r GG Y ი წმ R AGG L CAG r CTG E N AAC က ည E ကို ည က္ရွင္တ R AGG CIT F ACG R AGG ი მვვ FTTC CGG GAG ₩ IGG A S A GCC L V GTC CGG CAC TH ဗဗ္ဗ L ည် 4 D A GCC LCIT E V GTG ი მვვ Y S IATC T ACG P CCG M ATG E CAC L A GCC CAG V GTG L CHO CHO A GCC ACC CTG E GAG ဗ္ဗင္ဗ ი მვვ g G G R AGG CAC S AGC L CTG DGAC TACG RGC ы T ACC ₽ GCC D GAC I ATC A GCC s TCC CCG V GTC A GCC gg A E GAG s TCC K AAG L TTG r CTG GCC සු දු GAG CŢĠ ı TTG F TTT ACG က် ည V GTC gcc Gcc CGC CIC ဗ ၁ GAG ကို ည CAG ACC E ი გმ I ATC L R CTC AGG (F V GTC K AAG V GTG N AAC ACC E GAG A GCT DGAC ი მმ AAC AAC V GTC R AGG g gc I I ATT F CAG A GCG r G န ၂၄၄ Y TAT E GAA ACC. န TCC LCTT CCC CCC GAG R AGG Y ဗ္ဗင္ဗ CHC V A GTG GCC K AAG A GCC r CTG N AAC ССŢ E GAG G G G ကို ည CAC ACC ACC CAC E GAG GAG GAC ACG īg ≰ R AGG CAG A GCC s AGC CC P Þ ₩ TGG GAC CIC GAC ACG CTC r CTG E E K AAG D GAT CIC E V GTG r CTG က္ထင္တ cgg Sgg K AAG N AAC မှု CIG r GGC s TCC Y TAC g gg gcc Bcc ဗ္ဗင္ဗ ဗ္ဗဋ္ဌ r CTC S E A G န TCC K AAG ဗ္ဗဋ္ဌ

H ATC BGCC P CCC Y IAC g ggC F IATC V GTG E A r CTG T ACC CTA CAG r CTG E GAG M ATG F ი მმც ස වි EGAG CIGV GTC N AAC W TGG k AAG S AGC සි පි ₽ GCC r Agg GAG CIC M ATG GTG GCC GG P E GAG s AGC gg A o CAG CAG R AGG E P CCC V GTC V GTC DGAC R AGG r CTA M ATG F GAG A GCC A GCG s TCC F TTT CIG P D CCA GAC F N TTC AAC Y r CTC TTC ATC GCC GAG GAG GGG TGG CTA TTG ဂ ၁၅၅ T ACC CGG CIC **ရ** ၁၉၆ GAG K AAG K AAG S TCC E င္ပင္သင္တ R CGC r CGC E DGAC gcc V GTG H CAC E E V GTG CIC ₽ GCC H r CTG ACG M ATG M ATG L CTG H CAC A GCC IATT r CTG Y TAC M ATG V GTC ය පු D I GAC ATC rg CgC CGC CGC A GCT CAG gcc Bcc , P s TCG F T ACC A GCC GAG (D GAC MATG r CTG ₽ GCC K AAG အ CGC L CTT V GTG V GTG CGG Q CAG GAG A GCC AAG V GTG ဗ္ဗဗ္ဗ မှ ငရင် CIC gcc IATT A GCG M ATG ი მჭჭ Y TAC ₹ ೮ 9 9 9 9 r Agg GCC E GAG M ATG E CTC CIC F CIC E GAG E GAG GAG ¥ TGG R AGG A GCG gcc R CGG CTC DGAC E GAG CAG റദ്ദേ V GTC E GAG A GCC GCC R AGG CGG I ATA Y TAC T A GCC ත විවි F မှ သ ය ශීශීශී r GGG V GTG E V E GTG GAG K S AAG AGC F CCT GCC M ATG ATC CGC CAG V GTC V GTC V GTG K AAA IATC ACC. s AGC တ္မွင္လ AAC K AAG GAA CCA සු පු

GAC V G I G GTG GTG ATA GGG GAG V GTG GAG r CTG မှ သ P L A V CCC CTG GCC GTG V Y GTG TAT (

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s
TCA
                                                                                                                                                                                                                 GAC
                                                                                                                                                                                                                                                                                  N G K T G R G A V S E K D A P K E L
AAT GGT AAG AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
L S A K E G I D G R G G G H H H CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT
                                                                                                                                            M V K V K F K Y K G E E K E V D T
ATG GTG AAG GTC AAG TAT AAG GGT GAA GAA GAA GTA GAC ACT
                                                                                                                                                                                                              K I K K V W R V G K M V S F T Y D AAG ATA AAG ATT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC
                                                                                                                                                                                                                                                                                                                                                               *
TAG
                                                                                                                                                                                                                                                                                                                                                             L D M L A R A E R E K K // TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
                                                                      ::
                                                                        H H
CAT CAT
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Figure 17PP

Pfu DNA Polymerase (WT) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 69) ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc

aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag tagagocota tatocotoga ttataattac ccacaatgtt totocogata ototaaatot tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg gaaggagoto gaagaaaagt ttggatttaa agtoototac attgacactg atggtotota tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctcttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tentecenga aagattgaga tgttcttgg // // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Figure 17QQ

Sac7d - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA AGA AAA AAA AAA // ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc totaacctgg gttatagtga caaaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cotcccctat tttctctctt atgagatttt taagtatagt tatagagaag taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt tagagocota tatocotoga ttataattac coacaatgtt totocogata ototaaatot tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg

gaaggagoto gaagaaaagt ttggatttaa agtoototac attgacactg atggtotota tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag gggattette gttacgaaga agaggtatge agtaatagat gaagaaggaa aagteattae togtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa aggogatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttott ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

REPLACEMENT SHEET

FIGURE 1700 (CONT.)

ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagata gatgctacct aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgetteece aggaatgagg ttgttgtage tenteeenga TGA aagattgaga tgttcttgg //

Figure 17RR

Sac7d - pfu dna polymerase (v93 r or e) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 27) Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

FIGURE 17RR (CONT.)

GAC GAC GAT GCT CCA AAA GAA TTA GAA GTA GAC ACT TCA TTT ACC TAT TCC AAA GAG TGG AGA GTA GGC AAA ATG GTG GCA GAA AGA GAG AAG AAA AGC GAG AAA GGT GAA GTA TAT AAG GGA GCT AAG TIC AGA AGA GGT AAG ATA AAG AAG GTT GTA AAG TTA GCA ACA GGT AAG AAG TTA GAC ATG AAT

1020 1320 1380 1440 1500 1680 1800 1080 1140 1200 1560 1740 1260 099 540 009 720 780 840 900 960 CATTTACGCT AAGGCATGGA CAAGCCTATT AAAGAGATAC TGGACAACCT ACTTAGGAAA TCAAAGAAGG GTGGGAAAAC GCTATTCAAA AGAAAAGTT TCTTGCCTTC TATAATGATT TCTTCCATAC TATCAGGGAG ATATTTAGCG CGAGCCCAAG TTTCGACTTG TGTATATGAA AGCCTGGGAA GGCAACTTAT CAATGITICI AGTAGGCCAC GTTAGAGGAA AATACTCCTT TTATGGCTAT GGGAAGAAAG CCTCTACATT AAAGAAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA TGAAGAAGCT ACCAGAGAAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG TAACGGGGGA CCACTATTAG TTCCATTTGC GGGGAAGAAG AGCTAAAGAT TTCTCAGGAT GGAGACTCAT TCGCATTCCC TACGCCGACG AGATAGCAAA TCGCTCCTCA TCTACGGATA GAGATTGGAG ATGAAATTCC TTAGACCATA AAGGCCCAAT AAAACATAGA GAGATGGAAG GAAGAATACA CACTAGAGGC AAGATGCAAA CAAGATTAGT AGTGGTTCTT TGGATTCGTT AAAGAGCCAG AAAAGGGGTT TAATTACCCA TGGGACATTT GGTATGCAGT ACGGAGATGT AGTTTCTCGG AAGAGGAGTA CTATAGAAAA TTACTGCCTG GATTTAAAGT GTGAGGAAAT GACTGCTAGA GAAAATTTAA GATAGAGCAT GATAGAACTT AAGCCAAGTG GATTGAAGAA GTTAAGAAAA GAGTTTGGAA ATTACTTGGA GAGAGATG ATAAAGAGAT AGTIGCCAAA TACICGAIGG AACCTTGTAG CCCTCGATTA TGGTTTAGAG ATAGTTAGGA TAAAAGAAGT AATACAAAAG CTTGCCAATT TGTAGAGAG GTTGAGAAAA GGAACATCCC CAAGATXXXC GAATACGATA ACCATTGGAA GAAGTCAAGG CCAACATACA TCCAATGGAA ATTCAGCTTT AACTATGATA CCAAGTCTCT ACTCAAGATC GCAAATTCTT GCTGAGAGCG GAAAAGTTTG GGAGGAGAAA AAGCTCCCTG ATTCTTCGTT ACGAAGAAGA TTTGGAGACA ATACTAAAAC GGACATCTTC ACCAATGGAG CGAAGGAGAA AGCAAAGGTG GATTAAATTA GGAGAAGGTA AAGCACAGGG AGCTCCAAAC AGCCCTATAT GGGATGCAAG AATGAAGGAA AAAACTCTTA TACTTATAAT GACGGCTGTA AATAAATCTC TGGTTTTATA TAAGGAGTGT GGAGCTCGAA AACTATCCCA CATAAATTCA ATGATTCAAA CAGCAGTTGT GAATTGTTGA AACTTTATTT AAGGCCTAAT CCCTCTATCA ATGAAAATGA TATCAAGCGA AAAAACTTGG TAGGCGATAT TAACAAGGAC ACCTTGAGAG AAGAATTCCT TTTCAAGGTC GAAACGAAGT GCTACACAGG TAGATTTTAG TAAATCTTGA TTAAGACAAA AAAAAGCGAT GATGGTACTG GTCTCTATGC ATAAGAGGG TCATTACTCG AAGCTAGAGT ACATTATAGT GAAAGCCAAA AGGACATCCC TAGTATGGAA TTGTAAAATA ATGATTTAG CTCATCGACA AGTGGAGAGA CTCAGGGAGA GAAGGAAAAG **STGAGAATAG** AAAGAGAACG CTTCTCAGGG ACCGTGTGGA AGAGAACATC GATATAGAAA AGTTATGCAG AAGGATCCTG GCAATTTTG GAACTCGGGA TTATGGGATG GACTATAGAC GACACTGATG AAAGAAACTC AAGATTGTGA GTTGAGGTTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCCTACGAAA ATAGTATACC CCCGATACTC AAGTTCTGCA AGACAAAAGA GCAAAAGCAA TACATCGAGT GCTCTAGAAT GAAGGGTTTT

FIGURE 17RR (CONT.)

2100 2160 2220 2280 GAATATTACA TGGAGAACCA GGTTCTTCCA AATGGTAATT AGCTGAGGAA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC TAAAGCCAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT TICCIGGCII AACAITAAAA AAICC // GGAGTTAAAA GTATGACGCA AGCTGCTAAA GGATACATAG TACTTAGAGG CAAAGAAACT TACGATCCCA AAAAGCACAA GGATATTGGA TCGGCCTAAC ACAAGACAAG GCGGTACTTA GTAGCTGTTG

Figure 17SS

PPU DNA POLYMERASE (V93 R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 900 9 CTGTTATTAG GCTATTCAAA TTAGACCATA CATTTACGCT TAACGGGGGA AAGGCATGGA AGAAAAGTT TTCCATTTGC AAAGAGATAC TCTIGCCTIC TCTTCCATAC TATCAGGGAG TCGCATTCCC ATATTTAGCG CGAGCCCAAG TGTATATGAA AGCCTGGGAA CAAGATTAGT TGGACAACCT CAAGCCTATT TATAATGATT TTTCGACTTG GGCAACTTAT GLUTAMIC ACID) CCACTATTAG GGGGAAGAG AGCTAAAGAT AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA AGTTTCTCGG AAGGCCCAAT AAAACATAGA TTCTCAGGAT GAGATGGAAG GAAGAATACA CACTAGAGGC AGATAGCAAA V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT GTTAAGAAAA GTTGAGAAAA GAATACGATA GAGTTTGGAA ATTACTTGGA ATAAAGAGAT TACGCCGACG TCCAATGGAA ATTCAGCTTT CAAGATXXXC GGAGACTCAT ACCATTGGAA GAAGTCAAGG CCAACATACA GATTGAAGAA TGTAGAGAAG ACCAATGGAG GAGAGAGATG GATTAAATTA GACGCCTGTA GGAACATCCC GGACATCTTC CGAAGGAGAA AGCAAAGGTG TACTTATAAT AATAAATCTC GGAGAAGGTA ATGATTCAAA GAATTGTTGA AAGGCCTAAT CCCTCTATCA TAACAAGGAC SAACTCGGGA AAGAATTCCT AACTTTATT CAGCAGTTGT ATGAAAATGA TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT GAAAGCCAAA CTTCTCAGGG CTCATCGACA AGTTATGCAG AAGGATCCTG AAAAGGGCAG TATCATGTAA SCAATITITG AAGATTGTGA ACCGTGTGGA AGAGAACATC SATATAGAAA GTTGAGGTTG ATGCAGAGAA

FIGURE 17SS (CONT.)

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1260
                                                        1320
                                                                      1380
                                                                                    1440
                                                                                                  1500
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                                                                                                                             1620
                                                                                                                                           1680
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                                                                                                                                                                        1800
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                                                                                                                                                                                                    1920
                                                                                                                                                                                                                  1980
                                                                                                                                                                                                                               2040
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                                                                                                                                                                                                                                                            2160
             1140
                                                                                                                                                                                                                 ACCAGAGAAG
                                                                    GTTAGAGGAA
                                                                                                                                                                                                                               AGGTCCTCAC
                                                                                                                                                                                                                                                            AGCTGAGGAA
                                                                                                                                                                                                                                                                         GGTTCTTCCA
ACTTAGGAAA
             TCAAAGAAGG
                            GTGGGAAAAC
                                         CAATGITICI
                                                        AGTAGGCCAC
                                                                                   AATACTCCTT
                                                                                                 TTATGGCTAT
                                                                                                               GGGAAGAAAG
                                                                                                                             CCTCTACATT
                                                                                                                                          AAAGAAAAG
                                                                                                                                                          GCTTGAATAT
                                                                                                                                                                        AATAGATGAA
                                                                                                                                                                                      TGAAATTGCA
                                                                                                                                                                                                    TGAAGAAGCT
                                                                                                                                                                                                                                             AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT
                                                                                                                                                                                                                                                                                      TACAGAAAGG AAGACCTCAG ATACCAAAAG
AACCTIGIAG AGIGGIICTI
                                                       TCGCTCCTCA
                                                                                                                                                                      GGTATGCAGT
                                                                                                                                                                                     GAGATTGGAG
                                                                                                                                                                                                  ACGGAGATGT
                                                                                                                                                                                                                 ATGAAATTCC
                                                                                                                                                                                                                              ATAAGGCGAT
                                                                                                                                                                                                                                                           GGCCAATTCT
                                                                                                                                                                                                                                                                        TGGAGAACCA
            AAGCCAAGTG AAGAGGAGTA
                                                                    TGGGACATTT
                                                                                   CTATAGAAAA
                                                                                                  TCTACGGATA
                                                                                                               TTACTGCCTG
                                                                                                                                          GTGAGGAAAT
                                                                                                                                                         GACTGCTAGA
                           AAAAGGGGTT
                                          TAATTACCCA
                                                                                                                             GATTTAAAGT
                                                                                                                                                                                                                                                                                                    TICCIGGCII AACAITAAAA AAICC //
                           AAAGAGCCAG
                                                                                                                                                                                                   TTTGGAGACA ATACTAAAAC
                                                                                                                                                                                                                                                                        GTATGACGCA GAATATTACA
                                                       GGGATGCAAG AACTATGATA
                                                                                                               GCTGAGAGCG
                                                                                                                             GAAAAGTTTG
                                                                                                                                          GGAGGAGAAA
                                                                                                                                                        AAGCTCCCTG
                                                                                                                                                                       ACGAAGAAGA
                                                                                                                                                                                     TGGTTTAGAG ATAGTTAGGA
                                                                                                                                                                                                                 CTTGCCAATT
                                                                                                                                                                                                                               TTACATGAGT
                                                                                                                                                                                                                                                          CGATGGTCCA ATTAGCAATA
                                          CCCTCGATTA
                                                                    CCAAGTCTCT
                                                                                   ACTCAAGATC
                                                                                                  GCAAATTCTT
AAGCACAGGG
                                                                                                                                                                                                                                                                                       GGGATTTGGA
                                        AGCCCTATAT
                                                                                   AATGAAGGAA
                                                                                                                                          AACTATCCCA
                                                                                                                                                         CATAAATTCA
            AGCTCCAAAC
                                                                      TGGTTTTATA
                                                                                                  AAAACTCTTA
                                                                                                                             GGAGCTCGAA
                                                                                                                                                                        ATTCTTCGTT
                                                                                                                                                                                                                 AATACAAAAG
                                                                                                                                                                                                                               AACAAGACCA
                            TGGATTCGTT
                                                                                                               TAAGGAGTGT
                                                                                                                                                                                                                                                                                                    ACAAGACAAG TCGGCCTAAC
TTTCAAGGTC
            GAAACGAAGT
                                        TAGATTTTAG
                                                                                                  AAAAAGCGAT
                                                                                                                             TAGTATGGAA
                                                                                                                                         GTCTCTATGC
                                                                                                                                                                        ATAAGAGGG
                                                                                                                                                                                     TCATTACTCG
                                                                                                                                                                                                                 TAAAAGAAGT
                                                                                                                                                                                                                               ATGAGCAGAT
                                                                                                                                                                                                                                            CAAAGAAACT
                                                                                                                                                                                                                                                           TACTTAGAGG
                                                                                                                                                                                                                                                                        AAAAGCACAA
                                                                                                                                                                                                                                                                                      GGATATTGGA
                            GCTACACAGG
                                                        TAAATCTTGA
                                                                      AGGACATCCC
                                                                                    TTAAGACAAA
                                                                                                               GATGGTACTG
                                                                                                                                                         TTGTAAATA
                                                                                                                                                                                                    AAGCTAGAGT
TTATGGGATG
                                        ATAGTATACC
                                                                                                 GACTATAGAC
                                                                                                                                         GACACTGATG
                                                                                                                                                                                     GAAGGAAAAG
                                                                                                                                                                                                                 GTGAGAATAG
                                                                                                                                                                                                                                            GTAGCTGTTG
                                                                                                                                                                                                                                                           GGATACATAG
                                                                                                                                                                                                                                                                        TACGATCCCA
                                                                                                                                                                                                                                                                                       GCGGTACTTA
             GCCTACGAAA
                           CTCAGGGAGA
                                                        CCCGATACTC
                                                                      AAGTTCTGCA
                                                                                   AGACAAAAGA
                                                                                                               GCAAAAGCAA
                                                                                                                             TACATCGAGT
                                                                                                                                                         GCTCTAGAAT
                                                                                                                                                                        GAAGGGTTTT
                                                                                                                                                                                                    AAAGAAACTC
                                                                                                                                                                                                                              CTCGCAATAT
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GAC TTT ACC TAT GAC CCA AAA GAA GTA GAC ACT GCT GAA GAA GAG AAA AGA GTA GGC AAA ATG GTG TCC GAG AAA GAT GAA AGA GAG AAG AAA // AAG GGT GCT GTA AGC TAT AAG GGA GCA TGG $_{
m TTC}$ AGA AGA ACA GGT GTA AAG AAG ATA AAG AAG GTT ATG TTA GCA AAG AAG GAC // ATG GTG AAT GGT

Figure 17TT

PFU DNA POLYMERASE (G387P/V93R OR E) - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)

FIGURE 17TT (CONT.)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1020 1140 1200 1260 1320 1380 1500 1560 1620 1680 1740 1800 1860 1080 1440 840 540 900 or T) TCAAAGAAGG CAATGTTTCT AGTAGGCCAC GTTAGAGGAA GTGAGGAAAT AAAGAAAAG TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT TAPAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG TTAGACCATA CATTTACGCT GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT TTTCGACTTG CACTAGAGGC TGTATATGAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA GTGGGAAAAC GGGAAGAAAG TGAAATTGCA ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA AGAAAAAGTT AAAGAGATAC TCTTGCCTTC TCTTCCATAC TATCAGGGAG ATATTTAGCG CGAGCCCAAG GGCAACTTAT TGGACAACCT AATACTCCTT TTATGGCTAT CCTCTACATT GCTTGAATAT AATAGATGAA CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC G387P Mutant (CCN is the codon for Proline where $N=C,G,\lambda$, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CCACTATTAG TICCALITGC GGGGAAGAAG AGCTAAAGAT GAGAGAGATG ATAAAGAGAT TTCTCAGGAT GAAGAATACA CAAGATTAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA GGGATGCAAG AACTATGATA TCGCTCCTCA TGGTTTTATA CCAAGTCTCT TGGGACATTT AATGAAGGAA ACTCAAGATC CTATAGAAAA TCTACGGATA GAGATTGGAG AAAACATAGA GGAGACTCAT TCGCATTCCC GAGATGGAAG AGTIGCCAAA TACTCGAIGG AAGAIGCAAA NGGATTCGTT AAAGAGCCAG AAAAGGGGTT TAATTACCCA TTACTGCCTG GATTTAAAGT GACTGCTAGA GGTATGCAGT GAATACGATA ATTACTTGGA ATTCAGCTTT CCCTCGATTA GAAAAGTTTG V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CAAGATXXXC ACCATTGGAA GACGGCTGTA GAAGTCAAGG CCAACATACA GCAAATTCTT GCTGAGAGCG GGAGGAGAAA CATAAATTCA AAGCTCCCTG ATTCTTCGTT ACGAAGAGA TGGTTTAGAG ATAGTTAGGA GATAGAACTT GATAGAGCAT AGCAAAGGTG TCCAATGGAA GGAACATCCC GGACATCTTC ACCAATGGAG TACTTATAAT GATTAAATTA AATAAATCTC AGCCCTATAT AAAACTCTTA GGAGCTCGAA AACTATCCCA TAAGGAGTGT CTTCTCAGGG ATGATTCAAA GAATTGTTGA TAACAAGGAC TTTCAAGGTC AGGACATCCC TTAAGACAAA GAAAATTTAA CAGCAGTIGI AAGGCCTAAT ATGAAAATGA ACATTATAGT AAAAACTTGG TAGGCGATAT GAAAGCCAAA ACCTTGAGAG AAGAATTCCT GAAACGAAGT GCTACACACC TAGATTTTAG AAAAAGCGAT GATGGTACTG GICICIAIGC TTGTAAAATA ATAAGAGGG TCATTACTCG AAGCTAGAGT AACTTTATT CCCTCTATCA TATCAAGCGA TAAATCTTGA TAGTATGGAA AAAGAGAACG AAGGATCCTG TTATGGGATG AAGTTCTGCA AGACAAAAGA GACTATAGAC AAAGAAACTC GTGAGAATAG AAGATTGTGA ACCGIGIGGA CTCATCGACA GATATAGAAA AGTTATGCAG AAAAGGGCAG ATGCAGAGAA TATCATGTAA AGTGGAGAGA GAACTCGGGA GCCTACGAAA CTCAGGGAGA ATAGIAIACC CCGATACTC GCAAAAGCAA GAAGGAAAAG AGAGAACATC GTTGAGGTTG GCAATTTTG TACATCGAGT GACACTGATG GCTCTAGAAT GAAGGGTTTT

FIGURE 17TT (CONT.)

AGCTGAGGAA 2160 GGTTCTTCCA TACAGAAAGG AAGACCTCAG ATACCAAAAG AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT CGATGGTCCA ATTAGCAATA GGGCAATTCT GAATATTACA TGGAGAACCA ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // GTATGACGCA GGGATTTGGA CAAAGAAACT TACTTAGAGG AAAAGCACAA GGATATTGGA TACGATCCCA GTAGCTGTTG GGATACATAG GCGGTACTTA

ACC TAT GAC GAC GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA GTA GAG AAA GAA GTG TCC TTT TGA GAA AGA GAG AAG AAA // ATG GAA AAG GGT G GTA GGA TTA GAC ATG TTA GCA AGA GCA AAG GTT TGG AGA GGT AGA AAG AAG GTA AAT GGT AAG ACA AAG ATA AAG ATG :

Figure 17UU

PFU DNA POLYMERASE (G387P/V93R OR E) - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG (ALL POSSIBLE CODONS FOR ARGININE) 300 G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T) CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT AIGAITITAG AIGIGGAITA CAIAACIGAA GAAGGAAAAC CIGITAITAG GCIAITICAAA AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT CCACTATTAG AGAAAAGTT AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CAAGATXXXC ACCGIGIGGA AACTITATIT GGAACAICCC

FIGURE 17UU (CONT.)

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1080
                                                                                                                                                                                                                                                    1320
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                                                                                                                                                                                                                                                                                                         1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2220
                                                                                                                                                             1020
                                                                                                                                                                                             GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
                                                                                                                                                                                                                                  TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                  1920
                                                                                                         840
                                                                                                                                                                                                              GCTACACAGTTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
                                                                                                                                                          CAAGATTAGT TGGACAACCT
                                                                                                                                                                            TITCAAGGIC AAGCACAGGG AACCIIGIAG AGIGGIICIT ACTIAGGAAA
                                                                                                                                                                                                                                                  GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC
                                                                                    GAAGTCAAGG GAAGAATACA TTTCGACTTG
                                                                                                        CACTAGAGGC TGTATATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTGAGGAA
CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT
                 AGCAAAGGIG AITACTIGGA AAAACATAGA TCTICCATAC
                                   TATCAGGGAG
                                                    ATATTAGCG
                                                                    GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG
                                                                                                                         GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA
                                                                                                                                         AGTIGCCAAA TACTCGAIGG AAGAIGCAAA GGCAACTIAI
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                                  GAGAGATG ATAAAGAGAT
                                                                                                        CCAACATACA
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GAC GAC GTA GAC ACT CCA AAA GAA TAT ACC GCT GAA TIT TGA $\mathbf{T}^{\mathbf{C}\mathbf{C}}$ AAA GAT GAG AAA GAA AGA GAG AAG AAA // GTG ATG GAG GAA GTA GGC AAA GCT GTA AGC TAT AAG GGT AAG AGA GCA GGA TIC TGG GGT AGA GCA AGA GLL AAG GTA AAG ACA TIA AAG AAG AAG ATG GAC ATG GTG AAT GGT AAG ATA TTA 1

SAC7D-PFU DNA POLYMERASE (D141A/E143A/V93R OR

E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 31) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 32)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

GAC GTA GAC ACT ACC TAT GAC CCA AAA GAA GAA GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT TTC AAG TAT AAG GGT GAA GAG AAA TTA GCA AGA GCA GAA AGA GAG AAG AAA // // ATG GTG AAG GTA AAG AAG ATA AAG AAG AAT GGT AAG ACA TTA GAC ATG

1020 //ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 480 540 009 840 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CCACTATTAG AGAAAAGTT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC AAGGCCCAAT TATAATGATT TCTTCCATAC TTCTCAGGAT TATCAGGGAG CGAGCCCAAG TTTCGACTTG TGTATATGAA AGCCTGGGAA TGGACAACCT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG GGCAACTTAT TCTTGCCTTC ATATTAGCG CACTAGAGGC TACGCCGACG AGATAGCAAA CAAGATTAGT GGGGAAGAAG AGCTAAAGAT TCGCATTCCC GAGATGGAAG GAAGAATACA ATTACTTGGA AAAACATAGA AAGATGCAAA GAGTTTGGAA ATAAAGAGAT GGAGACTCAT GAAGTCAAGG TACTCGATGG GGAACATCCC CAAGATXXXC ACCATTGGAA CCAACATACA ATTCAGCTTT ACCAATGGAG GAGAGAGATG CGAAGGAGAA AGCAAAGGTG TACTTATAAT GATTAAATTA GACGGCTGTA GGAGAAGGTA AGTTGCCAAA TCCAATGGAA AATAAATCTC TTTCAAGGTC CTTCTCAGGG ATGATTCAAA AACTTTATTT AAGGCCTAAT TAGGCGATAT TAACAAGGAC SCCTACGAAA GAAACGAAGT GAATTGTTGA CAGCAGTTGT CCCTCTATCA ATGAAAATGA TATCAAGCGA ACATTATAGT AAAAACTTGG GAAAGCCAAA ACCTTGAGAG AAGAATTCCT ACCGTGTGGA CTCATCGACA AGTGGAGAGA SAACTCGGGA **LTATGGGATG** AAGATTGTGA AGAGAACATC GCNATAGCNA AGTTATGCAG GTTGAGGTTG AAGGATCCTG AAAAGGGCAG ATGCAGAGAA **TATCATGTAA** GCAATTTTTG

FIGURE 17VV (CONT.)

1680 1740 1800 1860 1920 2040 2100 2160 2220 2280 TAGATITIAG AGCCCTATAI CCCTCGAITA TAATTACCCA CAATGITICI 1260 1440 1620 1980 GCTACACAGTTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 TCGCTCCTCA AGTAGGCCAC ACCAGAGAAG TGGGACATTT GTTAGAGGAA CCTCTACATT AAAGAAAAG GCTTGAATAT AATAGATGAA ATAAGGCGAT AGGTCCTCAC GGTTCTTCCA TACAGAAAGG AAGACCTCAG ATACCAAAAG GGGAAGAAAG TGAAGAAGCT AATGGTAATT CTATAGAAA AATACTCCTT TTATGGCTAT TGAAATTGCA AGCTGAGGAA TTACTGCCTG GAAAAGTTTG GATTTAAAGT GTGAGGAAAT GACTGCTAGA ACGGAGATGT ATGAAATTCC TGGAGAACCA TCTACGGATA GGTATGCAGT TAAAGCCAGG GGGCAATTCT GAGATTGGAG regeceraae rrecregeir aacarraaaa aaree // ATACTAAAAC GGGATGCAAG AACTATGATA CCAAGTCTCT CTTGCCAATT TTACATGAGT GAATATTACA AATGAAGGAA ACTCAAGATC GCAAATTCTT GCTGAGAGCG GGAGGAGAAA AAGCTCCCTG ACGAAGAAGA ATAGTTAGGA GGAGTTAAAA ATTAGCAATA AAAACTCTTA ATTCTTCGTT TTTGGAGACA TGGTTTTATA TAAGGAGTGT GGAGCTCGAA AACTATCCCA CATAAATTCA TGGTTTAGAG AACAAGACCA AGCTGCTAAA CGATGGTCCA GTATGACGCA GGGATTTGGA AATACAAAAG AGGACATCCC TTAAGACAAA ATGAGCAGAT TAAATCTTGA TAGTATGGAA GTCTCTATGC ATAAGAGGGG AAGCTAGAGT TAAAAGAAGT TACTTAGAGG AAAAGCACAA GGATATTGGA AAAAAGCGAT GATGGTACTG TTGTAAATA TCATTACTCG CAAAGAAACT GACTATAGAC AAAGAAACTC GTGAGAATAG CTCGCAATAT ACAAGACAAG CTCAGGGAGA CCCGATACTC AAGTTCTGCA AGACAAAAGA GCAAAAGCAA TACATCGAGT GCTCTAGAAT GAAGGGTTTT GAAGGAAAAG GTAGCTGTTG GGATACATAG TACGATCCCA SCGGTACTTA ATAGTATACC GACACTGATG

TGA

Figure 17WW

KOD DNA POLYMERASE - Sac7d fusion protein

Nucleotide sequence (SEO ID NO; 33) // Nucleotide sequence (SEQ ID NO; 69) Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69) 793R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 120 180 TIGAACCCIA CIICIACGCC CTGTCATAAG AATTTTCAAG CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG GAGACCAGTT CAGCGATAAG GGACAAGATA GLUTAMIC ACID) GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT BAGGICIGGA AACTCIACTT TACTCATCCG CAGGACXXXC ACGGTTGTAA CGGTTAAGCG

FIGURE 17WW (CONT.)

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GAC
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            GCTCGCCTTC
                           CCTTATGATA
                                            TCTCCCCTAC
                                                           TGTGAAGGAG
                                                                                        CGAGCCGAAG
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CAAGCGCTAC
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             GCCAATGGAA GGCGACGAGG AGCTGAAAAT
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                               GACATTGAAA
                                              AGCTACGCCG
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                                                                                                                                                                                                                                                                                                                                       ACCGACGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGATCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCCGACGA
```

Sac7d - kod dna polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// AIG GIG AAG GIA AAG IIC AAG IAI AAG GGI GAA GAG AAA GAA GIA GAC ACI ICA AAG ATA AAG AAG GIT IGG AGA GIA GGC AAA AIG GIG ICC III ACC IAI GAC GAC AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

1020 1080 1140 //ATGAICCICG ACACIGACIA CAIAACCGAG GAIGGAAAGC CIGICAIAAG AAIITICAAG 60 840 300 600 9 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120 CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180 GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT CAGCGATAAG GGACAAGATA GCTCGCCTTC TCTCCCCTAC TCCTCCGTGT TGTGAAGGAG CCTCAGGAAG CAAGCGCTAC CCTTATGATA CTATCTGAAA CGAGCCGAAG CTTCGATCTC CGTTTATGAA TACGCTGAGG AAATAACCAC AGCCTGGGAA GGTCACATAC CGGCCAGTCC GGCCAGAAGA TCACCCACAA CGTCTCGCCG GGCGACGAGG AGCTGAAAAT GAGTTCGCCG AGGGGCCAAT CGCTTGAGGC AAGATGCGAA CTCGCTTAAT TACCCTTCGC AGAACGTGGA TCGACTTCGC GACGGATACA GAGGGTTGTG GGGATGGAAG CAGCACTGGC AACCTCGTTG AGTGGTTCCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT SIGIACCIAG AITITAGAIC CCIGIACCCC ICAAICAICA TACTCATCCG CAGGACXXXC GAGTACGACA ATAACTIGGA GAGGGAGATG ATAAAGCGCT GAAGTGAAGG CCCACATACA TACTCGATGG CTATGTAAAA GAGCCCGAGA GGCGACAACT GCCCTCGGAA GCCCAGCTTT TGAGGGCGAG TGACATCTAC GCCAATGGAA GGCCAGGGTG AACCTACAAC GTTTGCCGTC GATAAACCTG GGAGAAGGTT AGTCGCCCGC TCCGATGGAG AATAAACTTC CTCCTGAAGG ACGATTCTGC CGGTTAAGCG GAGGICTGGA AACTCTACTT CAGCAGTTAT AGGGATTAGT CTCTCTACCA ACGAGGAAGG ACGITCICAL AAAAGCTCGG TAAGACGGAC GTCAGCCGAA ACCTTGAGAG AGGAGTTCCT TCTCCCGCTC GGAATGAGCT ATGAAGGAGG TCTCGACGGA TGGGCGACAG AAAGACCCGG CGAGAGCATC CTCATAGACA GACATTGAAA AAGCGCTGTG TATCCTGTGA CTCTGGGACG CGGCAGAGCT ACCCTTCTAA AGCTACGCCG GTTGACGTCG ATTCAGAGGA GCCGTCTTCG ACCGGCGAGA GAGCTTGGGA GCCTATGAGA

FIGURE 17XX (CONT.)

1740 1980 2040 2160 1440 1500 1560 1620 1680 1800 1860 1920 2100 2220 ITCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGG 1380 TTAAGGTAAT CTACAGCGAC GTGAGGCGTG ACTGGAGCGA GATAGCGAAA TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG GTCAAAATAC GCCCTGGAAC GGTGATAAGC CCCCACAGGT CGGCCACCGC GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT CGGCTATGCA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC AATACCIGGA GCCGAIGCIG AAACCGICAA AAAGAAGGCI CGAGTACGAG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG CGATACCGTT CGACGAGTTC CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG TCCCCACGTT AGACAGGITG GITIGAGIGC ITGGCIGAAG CCGAAGGGAA CI //TAG 2325 ACGGTTACTA GAGGGATTTA AAGGACTACA AGGCAACCGG CGCTTGAGCT GATCCTGGCA AACAGCTACT GATAGAGGAA AAGTACGGCT CTTCCGGGCG GGCGACAGGG SATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CAACGCCAAA CTTCGTCACG ACTTGAGATT TGGGAGGATA CGCGAGAGGA AGAAGAAGAT GGGCCATCAA TTTTGCCAC CAACGCGCGG AGCAGATAAC AGAGGTTGGC TACATCGIGC TCAAGGGCTC GTTGAGAGAA TTCTGAGAGC GGTACTGCAA CCATCAAGGA TCAAGTATAT AACGCGGCTT CGAGGGTTCT AGGATAGTCA AAGAAGTTAC GACCCGACGA AGCACAAGTA GTGATCCACG ACCGACGGAT ATGGAGTTCC SCCGTIGCCA CAGAAGATAA AGGCCCCCT GGCTTCTACA **FACAGGCAGA** ATAACGATGA GGCAAGATAA GAGACGCAGG

Figure 17XY

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG

FIGURE 17YY (CONT.)

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1500
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           GGGCAAAATA
                                      CCTTGCCTTT
                                                   AATAATGATT
                                                                TTTGCCGTAT
                                                                            TGTTAAAGAA
                                                                                         GTATCTCATA
                                                                                                      ACATCCCGAA
                                                                                                                 AATCCACTTT
                                                                                                                               TGAGGCAGTT
                                                                                                                                            TGCCGCTATA
                                                                                                                                                           TGCTAGGGCA
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                                                                                                                                                                                                                                                                               CGGCTATATG
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AAGGGAAGTT
                         CAAGCGTTAT
AATTTTGGG
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                                                 AGGCCGAGAT
                                                              AAAATATCGA
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           CAGCTATGCG
                       TACCCTTTGC
                                    AGCTTAAGCT
                                                                                                                   TCAAGGGTAG
                                                                                                                               CGTATACGCT
                                                                                                                                            CAGAGGAAAT
                                                                                                                                                                       AGCTGGCAAA
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                                                                                                                                                                                                                                                                                                                                  TTCCAGGTCT
                                                                             TTGTTCAAGT
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                                                                                                       GGGACAAAGA
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GTCAGGAAAA
           CAAGACXXXC
                        GAATATGACA
                                      GGAGACGAGG
                                                                             ATAAAGCGTT
                                                                                         GGGGACAATT
                                                                                                       GTCTTAGGAA
                                                                                                                    GCTGTGGAAA
                                                                                                                               AACCTCCCAA
                                                                                                                                             AAATTAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTCGAAGCG
                                                                             AAGAGAAATG
                                                                                         AACTTACAAT
                                                                                                                                                           GAAAAAACTA
                                                                                                                                                                       ATTCTTCCCC
                                                                                                                                                                                                 TGAACTTGCA
                                                                                                                                                                                                              CCTGGGAGGA
                                                                                                                                                                                                                          TTTCCGCAGT
                                                                                                                                                                                                                                        AAAAGAGGGC
                                                                                                                                                                                                                                                     CTTTCCGGGC
                                                                                                                                                                                                                                                                               GGCTATTAAA
                                                                                                                                                                                                                                                                                                                                                GAGAGGATTC
                                                                                                                                                                                                                                                                                                                                                                            AAAGGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                 AAGACTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAGGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACAAGTAC
TGCAGTGAAA
            CGAGCATCCC
                         TGACATTTAC
                                                   TGAGGGAGAT
                                                                                                                                             AACCAAAAGC
                                       TCCCATGGAG
                                                                                                        AGTICGGCTI
                                                                                                                    TGATAGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                  CGATAGCAAA
GAGTGCTCGA
                         CAGCTGTGGT
                                      AGGGCTTGAT
                                                    CGTTTTATCA
                                                                             TGTCCAATGA
                                                                                         ATGTGATAAT
                                                                                                                   AGAGGATGGG
                                                                                                                                              TTTTAGGAAA
                                                                                                                                                           AAGAAAGCAT
                                                                                                                                                                                    GGGACGTCTC
                                                                                                                                                                                                 ACGCGAGGAA
                                                                                                                                                                                                              GAACAACTTA
                                                                                                                                                                                                                            TTTATTTGGA
                                                                                                                                                                                                                                        ATACCCTTGA
                                                                                                                                                                                                                                                     TCTGCAAGGA
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             AGCTCATTTT
                                                                 ATGAAGAAGA
                                                                                                       AAAAGCTGGG
                                                                                                                                                                         TCGGGAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAAGCTCAA
                                                                AGTTATGCCG
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AAAACTGTGA
             GAAGTCTGGA
                         AGGGAACATC
                                                                                         AAAGACCCCG
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                                      CTCATAGACA
                                                   GATATTGAAA
                                                                              GTCGATGTTG
                                                                                                        AAACGGGCAG
                                                                                                                                 GATCTTTCC
                                                                                                                                               TATGAAGCAG
                                                                                                                                                                        ACGTATGAGC
                                                                                                                                                                                                   AGGGTGGCAT
                                                                                                                                                                                                                CGGCGCTTAA
                                                                                                                                                                                                                                                     GGATATAGGT
                                                                                                                                                                                                                                                                               ATGCTCGATT
```

Figure 17ZZ

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 35)

CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CGG, ggg' CGA, AGG, = AGA, V93R MUTANT: XXX

1020 1080 1140 1200 1380 840 900 999 900 GGCCAAAATA GTATCTCATA AGCCAGAAAA AGGTTTGTGG CTATAATCCG AATTTTAAG TATATATGCT GAGACATGGA AAGGGAAGTT CAAGCGTTAT CCTTGCCTTT AATAATGATT TTTGCCGTAT TGTTAAAGAA ACATCCCGAA AATCCACTTT TGAGGCAGTT TGCCGCTATA TGCTAGGGCA GCTGATAGGT GTATCTTTA AGAGTATAAA TCCGATAGTA GGACTTAATT TTCAGCCCTA TAAAGGGCGA AATTTTGGG AAAATATCGA TTGTTCAAGT GGGACAAAGA TCAAGGGTAG CGTATACGCT CAGAGGAAAT CAATGGAAGA CCATACTCGG CAGCTATGCG TACCCTTTGC GAATTTGGAA AGGGCGAGAT TTGATTTGCC AGCTGGCAAA CTGATGAGGA CAATAATAGT GGAGACGAGG AGCTTAAGCT TCGTGGAGTG ACGATGTTGC ATAAAGGCAA CATAACAAAA GATGGCAAGC GTCAGGAAAA GAATATGACA ATAAAGCGTT GGGGACAATT GCTGTGGAAA AACCAAAAGC AAATTAGGAG TTTATTCCCT GACCCTCATT CAAGACXXXC ATCACATGGA GTCTTAGGAA AACCTCCCAA GCCCAGTACT ATGGAAGCTG ACCGGCAACC CCGAACAAAC TATGTAAAAG CTGTACCCTT TGTAAGAATT AAGAGAAATG AAGGACGATA TGAGGGAGAT GAAAAAACTA GAGATCAAGC CTTTCCGGGC TATTGAGGAG CGAGCATCCC TGACATTTAC TCCCATGGAG GGCCAGAGTA AACTTACAAT ATTCTTCCC CCTGGGAGGA AAAAGAGGC AATAGAACTT AGTTCGGCTT TGATAGTTT TGAACTTGCA TTTCCGCAGT TGCAGTGAAA ACACTGATTA CAGTIGIGCG GGGAGTTTAA ATGACTCCGC TGTCCAATGA ATGTGATAAT AGAGGATGGG TTTTAGGAAA GAGTGCTCGA AGCTCATTTT CAGCTGTGGT AGGGCTTGAT CGTTTTATCA AAAAGCTGGG AAGAAAGCAT TCGGGAAGGA GGGACGTCTC ACGCGAGGAA GAACAACTTA TTTATTGGA ATACCCTTGA TCTGCAAGGA ATGAAGAAGA AAAGACCCCG TGGGAAACAG AGGGTGGCAT GGATATAGGT ATGATACTGG CTTCTCAAAG AGTTATGCCG AAACGGGCAG TATGAAGCAG GTATCCCCAG AAAGAGAACG AAAACTGTGA GAAGTCTGGA AGGGAACATC CTCATAGACA GATATTGAAA GTCGATGTTG CCCAAGATTC SATCTTTCC ACGTATGAGC CAAAGTGTAT CGGCGCTTAA GAAAATATCA

FIGURE 17ZZ (CONT.)

1920 1560 1620 1680 1740 1800 1860 1980 2040 2100 2160 CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA GCTTGAGCTT TGCAGTCATA AAGTGTTGAA AATTTTACTT ITGCCGGCAG TACTIAGGAT ACTCGAAGCG TITGGATACA GAAAGGAGGA TITAAGGTAT CGGCTATATG CGCATGGGGG TAAGGTTCTT TTGGAGTGAG GGTTCCACTT AGCCATTGGC ACCGGGCACA AAACCAAGTT CGAAAAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AGGACTACAA ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TITGITACAA AAAAGCGCTA TAAGGAGAGA GAGGCTATAC TTAAAGAGGG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG AAGACTTGCC GCAAGAGGGA TAAAAGTGAA CAAAGGGAGC GGAAAGATAA GCGATAGGGT AAATCCACAA TTGACCCGAT GTACTCGAAG GAATGTGCTG AAAGCGTTAC AAACTACATA AACTCCAAAC TTCCAGGTCT CTTAGATGCA TGGCTCAAGA GG 2325 // TTGGAAGTAG AGGGATTTAA GCAGATTACC SCAATGAGGC AAGATATAAA GAAGAAAATG GAGAGGATTC AACAAGGGGC AAAGGTTTTA AGGCAAGATG ATCCTAGAAA CAAAGCTCAA AACAAACCGG AGGAATTCCT AGACTCAGGC TTATCCATGA ATATCGTTCT CGATAGCAAA TAGAGATGAC GCAGGATAAC GCTTTTACTT ATAATAAGCT ACAGAATACG AAAGCTGTAG ATGCTCGATT GGGTATCCTA TATGCGGACA GAGTATGAGG ATAGCTAAGG GAAAAGCTTG CCTCATGTCG AGACACTACA AAGAAAGCCA GATGAAGAGG

GAC TIT ACC TAT GAC GCT CCA AAA GAA GAA GTA GAC ACT AGA GTA GGC AAA ATG GTG TCC AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // GAG AAA GAA TAT AAG GGT AAG $_{
m TTC}$ AAG AAG GTT TGG GTA AAG AAG AAT GGT AAG ATA TTA GAC // ATG GTG

Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein

// Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 38)

FIGURE 17AAA (CONT.)

NS FOR ARGININE)	09	120	180	240	300	360	420	480	540	009	099	720	780	840	006	096	1020	1080	1140	1200	1260	1320	1380	1440	1500	1560	1620	1680	1740	1800	1860	1920	1980	2040	2100	2160
POSSIBLE CODONS ACID)	GATTTTCAAG	CATTTACGCT	GAGGCATGGG	GAGGCCGATT	GGATAAGATA	GAAGAGGTAC	GCTCGCATTT	TATAATGATA	TCTCCCGTAC	GATAAGGGAG	CTATCTAGTT	TGAGCCAAAG	CTTTGACCTC	AGTTTATGAG	GGCCTGGGAG	GGTAACGTAC	CGGCCAGCCC	CCTCAGGAAG	CGAGAGAAGG	CTGGGAGGGG	_			-	TTATGGGTAC	GGGGAGGGAA	CTTATACATA	AAAGAAGAAA		GATAGATGAG	CGAAATAGCC	TGAGGAGGCA	TCCAGAAAAG	AGGTCCGCAC	CATGGTGATA	TGCAGAGGAG
CGT (ALL GLUTAMIC	CGATTATA	TTAGACCTTA	TAACCGCCGA	AGTTCCTGGG	CCGCAATAAG	TICCGIICGC	AGCTCAAGTT	AGGGGCCCAT	AAAAGATCGA	TCCTCAAGGT	TCGACCTTCC	GGGACGGTAG	GAAGGATACA	CCCTCGAGGC	AGATAGCTGA	AGGATGCAAA	CAAGGTTAGT	AGTGGTACCT	AGAGGGAGTA	AGAAAGGGCT	_	•	-	CAATCGAGAA		TTACGGCCTG	_	CCGAGGAGAT	GGCTGTTGGA	AGTATGCGTT	GGGACTGGAG	ATGGCAACGT	ACGAMATACC			GGGCTATCCT
CODONS FOR		GACAGAAACT	GTTAGGAAGA	GTAAGGAAGA	CAGGACXXXC	GAGTACGACA	GGCGATGAAG	GAGTTCGCGA	ATAACGTGGA	ATAAAGCGGT	GGCGATTCTT	CCCCTGGGAA	GAGATAAAGG	CCAACATACA	TACGCTCACG	TATTCAATGG	GCCCAGCTTT	AACTTGGTGG	AAGCCGGATG	AAGGAGCCGG	_	_	CCCAGCCTGC	TCTAAAGACC	GCAAACAGCT	_	_	GGGGCAAAAC	AAGCTCCCAG	ACGAAGAAGA	ATAGTCAGGA	ATCCTAAAGC	CTGAGCAAGT	_	-	ATAAGCAAGA
A, AGG, CGA, A, GAG (ALL	ATCAC	GGTTGAGTAC	GATTGATGAG	TGCCGAAAAG	TGAACACCCT	TGACATCTTT	TCCAATGGAA	CGAAGGGGAG	AGCCAAAGTC	GAGGGAGATG	TACCTACAAC	GATAAAGCTA	GACAGCGGTG	GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG	TTCAACTGGC	GGCTCCAAAC	GGGATACGTT	GAGCCTGTAC	AGGGTGTAGG	GGGGTTTATC	GATGAAAGCT	CAAAATCCTG	TAAGGAGTGC	GGAACTGGAG	CACAATICCI	TATAAACGCC	GTTCTTCGTG	GGGGCTTGAA	CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA
$\Gamma: XXX = AGA,$ $\Gamma: XXX = GAA.$	ACGCTGA(GCGAGTTTAA	ATGACTCGCA	GAATTATAGA	GGCTGTACTT	CCGCAGTTAT	AAGGCCTAAT	CCCTCTATCA	ATGAGGAAGA	TTTCCAGCGA	ATGTTATAAT	AAAAGCTCGG	TTGGGGATAT	TTAGGAGAAC	GAAAGCCAAA	GACTGGAGAG	GGGAGTTCTT	TTTCTAGGTC	GGAATGAATT	GCTACGCTGG	TAGATTTCAG	TGAACAGGGA	AGGACTTCCC	TAAAAAGGAA	AACGGGCAAT	GTTGGTACTG	TCGTAAGGAA	GACTCTACGC	TCGTAGATTA	ACGTGAGAGG	TAATCACTAG	AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG
V93R MUTANT:		AAAGAAAACG	CTCCTCAAAG	AAGATAGTGA	GAGGTATGGA	AGAGAGCATT	CTAATAGACA	GACATAGAAA	AGCTATGCTG	GTCGAGGTAG	AAAGATCCCG	AAGAGGGCCG	ATGCAGAGGC	TACCACGIGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA	CTGTGGGATG	GCCTACGAGA	CTAAGGGAGA	TTAGTTTCCC	CCGGATACGC	AAGTTCTGCA	AGGCAAGAAA	GATTACAGGC	GCAAAAGCCC	TATATAGAGT	GACACAGATG	GCCCTAGAGT	GAGGCCTTCT	GAAGGGAAGA	AAAGAAACCC	GTAAAGATAG	CTAGTTATTT	GTTGCCGTGG	GGGTACATAG

FIGURE 17AAA (CONT.)

	TCA GAC TTA
2220 2280 2328	ACT GAC GAA
AG	GAC TAT AAA
TTAC	GTA
GGTT	GAA TTT GCT
TCAG CAG	AAA TCC GAT
AAAA ACCI	GAG GTG AAA
TAG AAG	GAA ATG GAG
TACP	GGT AAA AGC
GTAT	AAG GGC GTA
F 2 F 4	TAT GTA GCT
ACGCTTGG	AAG AGA GGA
STATE SGCCT	TTC TGG AGA
MGA O	AAG GTT GGT
AGCA)	GTA AAG ACA
GGAJ GAAJ CAGC	AAG AAG AAG
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG //	// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GGA GAA AGA GAA AAGA AAA GAA TTA
SGTTC	ATG AAG AAT
TT GC PC	>

Figure 17BBB

Sac7d - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

9 300 360 420 480 540 600 999 840 900 960 1020 1080 240 720 780 1140 1200 1320 //AIGATACTIG ACGCIGACTA CAICACCGAG GAIGGGAAGC CGAITAIAAG GAITITCAAG AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG GATAAGGGAG CCCTCGAGGC AGTTTATGAG CGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC CCGCAATAAG GGATAAGATA GAAGAGGTAC CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA TCTCCCGTAC TGAGCCAAAG GGCCTGGGAG GGTAACGTAC CGGCCAGCCC CCTCAGGAAG CGAGAGAAGG AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT GCTCGCATTT CTTTGACCTC CTATCTAGTI TTCCGTTCGC TCCAATGGAA GGCGATGAAG AGCTCAAGTT AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCCTCAAGGT GGGACGGTAG AGATAGCTGA AGGATGCAAA CAAGGTTAGT TICAACIGGC AACTIGGIGG AGIGGIACCI GGCTCCAAAC AAGCCGGATG AGAGGGAGTA TAATCACCCA GAAGGATACA TCGACCTTCC AGAAAGGGCT AGTIGCAAAG TATICAAIGG CAGGACXXXC GAGTACGACA GAGGGAGATG ATAAAGCGGT CCCCTGGGAA GAGATAAAGG TACGCTCACG CCCAATGGAG GCCCAGCTTT GGGATACGTT AAGGAGCCGG CCCTCGATAA GGCGATTCTT CCAACATACA TGAACACCCT TGACATCTTT TACCTACAAC GATAAAGCTA GACAGCGGTG GGAGAAAGTT GAGCCTGTAC GATAAACCTC CTCCTCAAAG ATGACTCGCA GGCTGTACTT CCGCAGTTAT AAGGCCTAAT ATGAGGAAGA TTTCCAGCGA ATGTTATAAT AAAAGCTCGG TTGGGGATAT TTAGGAGAAC GAAAGCCAAA GACTGGAGAG GGGAGTTCTT TTTCTAGGTC GCTACGCTGG TAGATTTCAG CCCTCTATCA GGAATGAATT CTAATAGACA AGCTATGCTG AAGAGGGCCG AAAGATCCCG ATGCAGAGGC GCAATCTTCG ACTGGAAAGG GCCTACGAGA TTAGTTTCCC GAGGTATGGA AGAGAGCATT GACATAGAAA GTCGAGGTAG TACCACGTGA SAGCTCGGTA CTGTGGGATG CTAAGGGAGA

REPLACEMENT SHEET

FIGURE 17BBB (CONT.)

AAGTTCTGCA	AAGTICIGCA AGGACTICCC GGGGTTTAIC CCCAGCCTGC ICAAGAGGTT	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA		GGAACTGGAG GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCT	CACAATICCI GGGCCAAAAC CCGAGGAGAT AAAGAAGAAA	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA AGTATGCGTT	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	ATAGTCAGGA GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG		TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG		AGACGGCCA ATAAGCAAGA GGGCTATCCT	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA		GGAAGCATAA GTATGACGCT GAGTATTACA	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG		TACAGGAAAG AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	ACTAAACAGA CAGGICTTAC GGCAIGGCIT AACAICAAGA AGAAG IAA	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17CCC

JDF-3 - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCCGATGGAAGGTGAGGAGGAGAGCTTAAACTCATGTCCTTCGAGATCGAGACGTCTACCACGAGGGGAGAAGAGTTTGGAA ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGAGGGGACGCGCGGGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAGTTCCTCGG CA GGTCTGTGGA GGTCTGGGTCCTCTA CTTCACGCA CCCGCA GGA CXXX CCGGCAA TCCG CGA CAAAA TAA GGAA GCA CCCG CGGGTCA TCGA CATCTA CGA GTA CGA CA TA CCA GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGGCGTGCTGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGA **ACCCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACATAA** ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCTTACTACTTCT ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGGGTTTGAGAG

FIGURE 17CCC (CONT.)

acgecegtegetaceteaaggagecegagegggactgtgggacaatategtgtatetagactttegtagtetetaqeetteaateataateaeceacaaggtegecagatae GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGGCTTGAGATAGTCAGGCGCG CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTTCGATTACAGGCAACGGGCQATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT A TGCCAGGGCAAGA TGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGTTGAGGAAAAGTTCGGTTTTAAAGTCCT CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCGGCCTTCTC TIGGAGCGAGATAGCGAAGGAGAGCGCAGGCGTTTTIGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAAGCTGAGCTGAGCTAAA GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGCCCCGCACGTAGCCATAGCGAAGCGTTTGGCCGCAGAGGT CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC 3GTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA AGA AGA AGA AAG AAA AAA // TAG

Figure 17DDD

Sac7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA AGA AAG AAA // AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA

FIGURE 17DDD (CONT.)

ccttcgccaagcgctacctcatagacaagggcctaatcccgatggaaggtgaggaagcttaaactcatgtccttcqgaqatgagacgctctaccacgagggagaagagtttgg CTACGCCGGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCATAATCATAATCACCCACAACGTCTCGCCAGAT GGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTCGATTACAGGCAACGGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGG GTGTTAAAATCCGGCCCGGGACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGGAGTTCGACGACGACGAAGCAAGTACGA TGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGC TCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGGGATAACCACGCGCGGGGCTTGAGATAGTCAGGCG CTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGGAGAAGGTGAAAAAAGTTCCTC GGCAGGTCTGTGGAGGTCTTGGGTCCTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATCGACATCTACGAGTACGACATAC TTACCCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACTTTATCCAGTCATAAGGCGCACCAT AAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGGCTTGAG ACGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCGAGGTCACAAGTTCTGCAAGGACTTCCCGGGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAA CTATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTAAAGTC CTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATAATCCCAAACTGCCCGGCCTTTC aagcgcttcttgagggtcgttaaggaagaaggacccggacgtgataacatacaacggcgacaacttcgactacctgcaaaaaagcgctgtgagaagcttggcgtgagct A GGGT CGC GCCTACT CGA TGGA GGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTT //ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCTTACTT GCGTGGCTGAAGCCGAAGGAGAAGAAGTGA

Figure 17EEE

Synthetic Sso7d gene:

Nucleotide sequence (SEQ ID NO: 71) Amino acid sequence (SEQ ID NO: 72) A T V K F K Y K G E E K E V D I S K GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG I K K V W R V G K M I S F T Y D E G ATC AAC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC G G K T G R G A V S E K D A P K E L GGT GGC AAG GCG CCG AAG GAC GCG CCG AAG GAG CTG L Q M L E K Q K K CTG CAG ATG CTG GAG AAG AAG

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein

Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)

```
// A T V K F K Y K G E E K E V D I S K
// GCA ACC GTA AAG TTC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
                                                                                                                                        I K K V W R V G K M I S F T Y D E G ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
                                                                                                                                                                                                                                                                              G G K T G R G A V S E K D A P K E L GGT GGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
                                                                                                                                                                                                                                                                                                                                                                                                                L Q M L E K Q K K // CTG CAG ATG CTG GAG AAG CAG AAA AAG //
```

FIGURE 17FFF (CONT.)

V GTG AAG g 3gg r CTG ACC မှ ည д Б A AA Y W K AAG E L ī. CTG CIG ACC CTC ₽ GCC ACG AGC D GAC g GGG CAG CAG V GTC r G I ഗ CCC A GCC CTC ri Si CIC K AAG r CTC A GCC E GAC ი წმ s AGC K AAG V GTC T ၁၁၅ S AGC ₽ GCC A GCC GAC CIG E GAG ႕ ပ္ပ GGC CGC F CCC CCC G GGG CGG r CTC v GTG V GTC R CGG K AAG K AAG GAC CAC CAC R AGG CIT ¥ TGG R CGG D D GAC GAC ი მვი cīg A GCC F g GGC r CTG I r CTC r CTG N AAC E I ATC GGC 7 AAG 4 D A GCG E GAG V GTC F TTC V GTC GAC ဗ္ဗဗ္ဗ E A G Н Y K TAC AAG A L I K GCC CTC ATC AAG A GCG v GTC CAC g gg V GTG CAC Y s TCC ကို ည ri G Ω GAG F I ATC GAG GAG IATC Y K AAG E GAG K AAG 占 3 ი მცვ Y TAC Y TAC GGC SGC T ACC V GTC V GTG GAA GAC FITT K AAG r CIG ഗ ი მენ ဗ္ဗင္ဗ r CTC ස විව A GCG A GCG g ggc GAC W ი მვვ GGG BB R AGG Н CCC CCC Y CAG GAC Y TAC CIC P CCG s TCC E CTT T ACC A GCG D GAC CAA r CTG 4 GCC V GTG ი მმმ A GCC V GTC K AAG LCTT r CTG W TGG T ACG r CTG Ы E M ATG r CTG GCG GAC E R CGG GAA LCTC A GCC ₽ GCC K AAG N AAC Ω ი მვი A GCG CAC E E CAC မှ သ r CTC CAG CAG CCG K AAG GGG EGAG CAC g GGG G G G F TTT R CGC K AAG Y K AAG ACC Y r CTC ი მმმ Σ T ACT ဗ္ဗဋ္ဌ F GAC A GCG K AAG CII සු පු r F IATC GAC CTC I ATC A GCC V GTC D 3AC s AGC A GCC S TCC EGAG r CTG д ЗАС L A GCC A GCC ဗ ဗ္ဗ

FIGURE 17FFF (CONT.)

3CC နှင့် ဒ္ဓဋ္ဌ F R GGG V GTG IATC L GIT A A 3CC L L CTG K AAA V GTT r CFC Y r CTC Y TAC ත වි R AGG ပ္ပင္ပ ය ශීශීශ EGAG r S CGC CTT T ACG FTTC GAA ។ ភូមិ යි දි R AGG EGAG LCTT Y TAT s AGC N AAC GTGE R CGG E GAG භ ල DGAT CCT CTG M ATG R GGG W TGG gcc A GCC Ø AAG GAC H CAC භ ල A GCC EGAG GAC r CCC CCC A GCC S TCC r CTT GAG o c V GTG L DGAC CTG GCC GGC CGC r CTC မှ ည W TGG က ည A A A CŢĊ ${\rm M} \\ {\rm ATG}$ GAG CAC 999 A GCC CAC r CTC W TGG M ATG A GCC A GCC DGAC R AGG r CTG ဗ္ဗဋ္ဌ EGAG Ħ GAC E A GCC GAG s AGC P CCC မှ ည ri CTD ဗ္ဗဋ္ဌ A GCC န TCC සි දි GGG A GCC R CGG E \mathbf{TGG} င် နိုင်ငံ A GCC E GAG CAC r CTT r CCC CCC r CTG R AGG r TTG r CTG E K AAG T ACC E ი გენ GTC FTT V GTC ი გე P CCG A GCC igc BC AAG CTC TCC A A A > უ ცც T ACC E GCC A GCT GAG r CGC K G G G CTC R AGG GAG සි දි F F N AAC A GCG r G r CTG s TCC ය ය A GCG ဗ ညွှ L s TCC LCTC V GTC CTGs TCC E D GAC EGAG CTT R AGG L Y TAT E GAG R AGG GCC GCC r CTT ი ცვვ E GAT PCCT CCC V GTG GAG K AAG V GTG R AGG K AAG ဗ ဗ္ဗ ი წწ A GCC A GCC Д GAC GAG DGAC r CTG CCC A GCC CTG GAA T ACG W TGG AGG V GTG GAG F TTT œ ATG r CTG W TGG GAG CTG F S AGC ၁၉ A GCC GAC R AGG r CTG GAC r CTC GAG N AAC GTG CGC CGC gg A GAA v GTG A GCC R AGG L CTG r CTC r CTG မှ ည F L CTG CTC A GCC Y A GCC GAG r CGC A GCC r CTG R AGG L ი მმმ

FIGHRE 17FFF (CONT)

ACC A 3CC ACG S AGT R AGG Y TAT IATC F A GCC д ССС Y I ATC R AGG CAG GAC L CTG gcc Gcc E GAG r STC CIA M ATG T ACC LCTA F ი მმც Ggg GAG P CCC AGG g GGG GGC CGC $^{
m L}$ r CTG N AAC W TGG K AAG E S AGC R GGG R R AGG AGG CAC s AGC CIT V GTC GGG ဗီဗီင r CTT A GCC GAG A GCC CAG Q CAG CTA GAG ტ ტე I ATC Y TAC T ACG A GCC F TTT A GCC CCG V GTG D GAC A GCG S TCC E L GAG CTA P D L CCG GAC CTC A T A A ACG GCC R T CGC ACC L L CTA TTG E G I V E K I L Q ATC GTG GAG AAG ATC CTG CAG GAC ය ශීලී T S A ACC AGC GCC T R CGG r CTC Y TAC CCA GAG S TCC RGC GGC R R д F N Q T A TTC TTC AAC CAG ACG GCC V GTC T ACG TGG E GAG r CTC M ATG CAC E GTG > s TCC 1 H r TTG CCC CTG g GGG CAC A GCC I ATT r CIG CGC TAC × I D P ATT GAC CCC N I AAC ATC E E GAG GAG GCC CCC s TCG ACC. G K R GGC AAG CGC V L A GTG CTG GCC R D I CGG GAC ATC F r CTC ഷ K AAG P R R CGC CGC (GAC M ATG V GTC A GCC CAG R AGG A GCC V GTG ദേദ CAG E GAG L E CTG GAA A A H P GCC CAC CCC 1 L Y CTC TAC W I TGG ATT E K T GAG AAG ACC K S T Y AAG AGC ACC TAC CTC L R CTC AGG စ ဗိမ္မ ი მ<u>ვ</u>ი GCC R CGC I ATC GCC F TTC (T ACC F E GAG AAC GAG GAG CAC CŢC CAG CCC gcc Gcc E GAG CAG R CGG V GTC E GAG A GCC E GAG I ATA T ACC ACG D GAT r CTC ი მმმ R CGG GAC CGG F က် ည ¥ TAC G K GGC AAG CGC R r CTG CGC CGC S TCC R CGC CAG V GTC V GTC $^{\mathrm{F}}$ PCCT V GTG S CTC ာ ၁၁၅၅ K AAG AAC g GGC S AGC S AGC CGG IATC I K AAG

FIGURE 17FFF (CONT.)

ი მმე E GAG A GCC ი გვვ L E CTC GAG M E ATG GAG P V Q CCC GTC CAG CIG r AGG GCC V GTC V GTC R E A A E R M A F N M CGG GAG GCG GCG GCC GAG CGC ATG GCC TTC AAC ATG F r GTG R L A K E CGG CTG GCC AAG GAG D E GAC GAG K L AAG CTC L M K L A M V CTC ATG AAG CTG GCT ATG GTG CAC V GTC L Q CTT CAG A E A V A GCG GCG GCG GCG CTC R M AGG ATG E R DGAC A GCC gcc Gcc K S V AAG AGC GTG ი მ<u>ვ</u>ვ T A A A A A A C C GCC P K CCA AAA E M GAA ATG

W H E D GAG GAC L S A K E G I D G R G G G H H H CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT A V P L E V E V G I G GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG r CTG GCC CCC V Y GTG TAT

H H * CAT CAT TAA

Figure 17GGG

Pfu DNA Polymerase (WT) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 71)

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

FIGURE 17GGG (CONT.)

ttacataact gaagaaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt cottocaatg gaaattcago tttcaagatt agttggacaa cotttatggg atgtttcaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc tagagocota tatocotoga ttataattac coacaatgtt totocogata ototaaatot tcacgaagga

FIGURE 17GGG (CONT.)

atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac togtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa aggogatggt ccaattagca atagggcaat tctagotgag gaatacgato ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

FIGURE 17GGG (CONT.)

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct ttccggggagt tttgtattgc tctagccaag gtttggggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tentecenga acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct aagattgaga tgttcttgg //

ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC // GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG TGA = CTG CAG ATG CTG GAG AAG CAG AAA AAG

Figure 17HHH

PFU DNA POLYMERASE (V93 R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 1140 1200 1020 1080 1260 1320 1500 1380 1440 999 840 900 960 GTTAAGAAA TAACGGGGGA AAGGCATGGA CAAGCCTATT TATAATGATT TGTATATGAA GGCAACTTAT TGGACAACCT ACTTAGGAAA TCAAAGAAGG AGTAGGCCAC GGGAAGAAAG CATTTACGCT AAAGAGATAC TCTTGCCTTC CGAGCCCAAG TTTCGACTTG AGCCTGGGAA CAATGITTCI GTTAGAGGAA CCTCTACATT GICTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG AGAAAAGTT TCTTCCATAC GTGGGAAAAC AATACTCCTT TTATGGCTAT CTGTTATTAG GCTATTCAAA TATCAGGGAG ATATTTAGCG GLUTAMIC ACID) AGTTTCTCGG AGCTAAAGAT AAGGCCCAAT AAAACATAGA GAAGAATACA TITCAAGGIC AAGCACAGGG AACCIIGIAG AGIGGIICII AAGAGGAGTA TTAGACCATA CCACTATTAG TTCCATTTGC TTCTCAGGAT TCGCATTCCC CAAGATTAGT CTATAGAAAA GAGATGGAAG CACTAGAGGC AGATAGCAAA AAGATGCAAA AAAAGGGGTT TAATTACCCA TCGCTCCTCA TGGGACATTT TCTACGGATA TTACTGCCTG GATTTAAAGT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GTTGAGAAAA GGGGAAGAAG GAGTTTGGAA ATTACTTGGA GGAGACTCAT ACCATTGGAA GAAGTCAAGG CCAACATACA TACGCCGACG TACTCGATGG TCCAATGGAA ATTCAGCTTT AGCICCAAAC AAGCCAAGIG AAAGAGCCAG AACTATGATA GCTGAGAGCG GAAAGTTTG ATGATTITAG ATGTGGATTA CATAACTGAA GAAGGAAAAC GATAGAACTT CAAGATXXXC GAATACGATA ATAAAGAGAT CCCTCGATTA CCAAGTCTCT ACTCAAGATC GCAAATTCTT GAAAATTTAA GATAGAGCAT ATGATTCAAA GATTGAAGAA GGACATCTTC AGCAAAGGTG GACGGCTGTA GGGATGCAAG AATGAAGGAA TAAGGAGTGT GGAGCTCGAA TGTAGAGAAG ACCAATGGAG GAGAGAGATG TACTTATAAT GGAGAAGGTA AGTTGCCAAA TGGATTCGTT AGCCCTATAT AAAACTCTTA GGAACATCCC CGAAGGAGAA GATTAAATTA AATAAATCTC TGGTTTTATA AAGGCCTAAT ATGAAAATGA AAGAATTCCT TTAAGACAAA GATGGTACTG GAATTGTTGA TAGGCGATAT TAACAAGGAC ACCTTGAGAG GAAACGAAGT AGGACATCCC TAGTATGGAA AACTTTATT CAGCAGTTGT CCCTCTATCA TATCAAGCGA ACATTATAGT AAAAACTTGG GAAAGCCAAA GCTACACAGG TAGATTTAG AAAAAGCGAT TAMATCTTGA CTTCTCAGGG AAAGAGAACG AAGATTGTGA AGTTATGCAG AAAAGGGCAG GAACTCGGGA CCCGATACTC AGACAAAAGA GACACTGATG ACCGTGTGGA CTCATCGACA GATATAGAAA AAGGATCCTG ATGCAGAGAA TATCATGTAA AGTGGAGAGA CTCAGGGAGA ATAGTATACC AAGTTCTGCA GACTATAGAC TACATCGAGT AGAGAACATC GTTGAGGTTG TTATGGGATG GCCTACGAAA GCAATTITIG GCAAAAGCAA

FIGURE 17HHH (CONT.)

GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG TAC GAC GAG 2040 2100 1980 AGCTGAGGAA 2160 GAC ATC GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG GGATATIGGA GGGATITGGA TACAGAAGG AAGACCICAG ATACCAAAAG TGAAGAAGCT CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC AATGGTAATT TIGIAAAAIA CAIAAAIICA AAGCICCCIG GACIGCIAGA GCIIGAAIAI AATAGATGAA GGTTCTTCCA TGAAATTGCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAAGGGTTTT ATAAGAGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TTTGGAGACA ATACTAAAAC ACGGAGATGT CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG TACTTAGAGG CGAIGGICCA ATTAGCAATA GGGCAATTCT AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GTG GGC AAG ATG ATC TCC TTC TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC 2328 CTG CAG ATG CTG GAG AAG CAG AAA AAG CGI AAG ACC GGC CGT AAA GTA TGG AAGCTAGAGT TCATTACTCG ACAAGACAAG ATC AAG GGT GGC GGATACATAG TACGATCCCA GCGGTACTTA GCTCTAGAAT GAAGGAAAAG // GCA ACC AAAGAAACTC GTAGCTGTTG

Figure 17III

PFU DNA POLYMERASE (G387P/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 71)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 337P Mutant (CCN is the codon for Proline where N = C, G, A, or T) AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG ATGATITIAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA CAGCAGTIGI GGACAICTIC GAATACGAIA TICCAITIGC AAAGAGAIAC TATCAGGGAG AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG AAGGCATGGA CAAGCCTATT AGAAAAGTT TCTTGCCTTC TATAATGATT TCTTCCATAC V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGAA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT AGCAAAGGTG ATTACTTGGA AAAACATAGA GGAACATCCC CAAGATXXXC CCACTATTAG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, AAGGCCTAAT GAATTGTTGA AACTTTATTT CCCTCTATCA ATGAAAATGA TATCAAGCGA AGAGAACATC CTCATCGACA GATATAGAAA GTTGAGGTTG AAGATTGTGA ACCGTGTGGA AGTTATGCAG

FIGURE 17III (CONT.)

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1740
                                                                                1140
                                                                                                            1260
                                                                                                                          1320
                                                                                                                                      1380
                                                                                                                                                     1440
                                                                                                                                                                    1500
                                                                                                                                                                                  1560
                                                                                                                                                                                               1620
                                                                                                                                                                                                                                                     1860
                                                                                                                                                                                                                                                                                1980
                                                                                                                                                                                                                                                                                               2040
                                                                                                                                                                                                                                                                                                            2100
                                                                                                                                                                                                                                                                                                                          2160
                                                      1020
                                                                    1080
                                                                                               1200
                                                                                                                                                                                                              1680
                                                                                                                                                                                                                                         1800
                                                                                                                                                                                                                                                                    1920
TTTCGACTTG
                                                      TGGACAACCT
                                                                    ACTTAGGAAA
                                                                                                           CAATGITICI
                                                                                                                         AGTAGGCCAC
                                                                                                                                      GTTAGAGGAA
                                                                                                                                                                   TTATGGCTAT
                                                                                                                                                                                 GGGAAGAAAG
                                                                                                                                                                                                            AAAGAAAAG
                                                                                                                                                                                                                                       AATAGATGAA
                                                                                                                                                                                                                                                                   TGAAGAAGCT
                                                                                                                                                                                                                                                                                ACCAGAGAAG
                                                                                                                                                                                                                                                                                                                                        GGTTCTTCCA
                                                                                                                                                                                                                                                                                                                                                    ATACCAAAAG
              TGTATATGAA
                                         GGCAACTTAT
                                                                                TCAAAGAAGG
                                                                                               GTGGGAAAAC
                                                                                                                                                     AATACTCCTT
                                                                                                                                                                                               CCTCTACATT
                                                                                                                                                                                                                         GCTTGAATAT
                                                                                                                                                                                                                                                     TGAAATTGCA
                                                                                                                                                                                                                                                                                              AGGTCCTCAC
                                                                                                                                                                                                                                                                                                                          AGCTGAGGAA
                                                                                                                                                                                                                                                                                                            AATGGTAATT
                                                                                                                                                                                                                                                                                                                                                    TACAGAAAGG AAGACCTCAG
                                                                                                                                                                                                                                                                                                                                      GTATGACGCA GAATATTACA TGGAGAACCA
                                                                                                                           TCGCTCCTCA
GAAGTCAAGG GAAGAATACA
            CCAACATACA CACTAGAGGC
                          AGATAGCAAA
                                                     CAAGATTAGT
                                                                  AAGCACAGGG AACCTTGTAG AGTGGTTCTT
                                                                                AAGAGGAGTA
                                                                                              AAAAGGGGTT
                                                                                                                                      TGGGACATTT
                                                                                                                                                     CTATAGAAAA
                                                                                                                                                                   TCTACGGATA
                                                                                                                                                                                TTACTGCCTG
                                                                                                                                                                                              GATTTAAAGT
                                                                                                                                                                                                            GTGAGGAAAT
                                                                                                                                                                                                                                      GGTATGCAGT
                                                                                                                                                                                                                                                                   TITGGAGACA ATACTAAAAC ACGGAGATGI
                                                                                                                                                                                                                                                                               ATGAAATTCC
                                                                                                                                                                                                                                                                                              ATAAGGCGAT
                                                                                                                                                                                                                                                                                                           GGAGTTAAAA TAAAGCCAGG
                                                                                                                                                                                                                                                                                                                         GGGCAATTCT
                                         AAGATGCAAA
                                                                                                             TAATTACCCA
                                                                                                                                                                                                                         GACTGCTAGA
                                                                                                                                                                                                                                                     GAGATTGGAG
                                                                                                                                                                                                                                                                                                                                                                  TICCIGGCIT AACAITAAAA AAICC //
                          TACGCCGACG
                                        TACTCGATGG
                                                     TCCAATGGAA ATTCAGCTTT
                                                                                AAGCCAAGTG
                                                                                               AAAGAGCCAG
                                                                                                                                                                                              GAAAAGTTTG
                                                                                                                                                                                                                                                                                CTTGCCAATT
                                                                                                                                                                                                                                                                                              TTACATGAGT
                                                                                                                                                                                 GCTGAGAGCG
                                                                                                                          AACTATGATA
                                                                                                                                      CCAAGTCTCT
                                                                                                                                                                                                             GGAGGAGAAA
                                                                                                                                                                                                                         AAGCTCCCTG
                                                                                                             CCCTCGATTA
                                                                                                                                                      ACTCAAGATC
                                                                                                                                                                   GCAAATTCTT
                                                                                                                                                                                                                                                    TGGTTTAGAG ATAGTTAGGA
                                                                                                                                                                                                                                                                                                                          ATTAGCAATA
                                                                                                                                                                                                                                         ACGAAGAAGA
                                                                                                                          GGGATGCAAG
GACGGCTGTA
                          GGAGAAGGTA
                                                                                                           AGCCCTATAT
                                                                                                                                                      AATGAAGGAA
                                                                                                                                                                                                                                        ATTCTTCGTT
                                                                                                                                                                                                                                                                                                             AGCTGCTAAA
                                                                                                                                                                                                                                                                                                                          CGATGGTCCA
                                                                                                                                                                                                                                                                                                                                                     GGGATTTGGA
                                         AGTTGCCAAA
                                                                                              NGGATTCGTT
                                                                                                                                        TGGTTTTATA
                                                                                                                                                                   AAAACTCTTA
                                                                                                                                                                                TAAGGAGTGT
                                                                                                                                                                                              GGAGCTCGAA
                                                                                                                                                                                                             AACTATCCCA
                                                                                                                                                                                                                          CATAAATTCA
                                                                                                                                                                                                                                                                                AATACAAAAG
                                                                                                                                                                                                                                                                                              AACAAGACCA
                                                                                 AGCTCCAAAC
              AATAAATCTC
              TAACAAGGAC
                                                     AAGAATTCCT
                                                                                                                                                      TTAAGACAAA
                                                                                                                                                                                                                                                                                TAAAAGAAGT
                                                                                                                                                                                                                                                                                                           CAAAGAAACT
                                                                                                                                                                                                                                                                                                                         TACTTAGAGG
                                                                                                                                                                                                                                                                                                                                       AAAAGCACAA
                                                                                                                                                                                                                                                                                                                                                                  TCGGCCTAAC
                                         ACCTTGAGAG
                                                                    TTTCAAGGTC
                                                                                                                                      AGGACATCCC
                                                                                                                                                                   AAAAAGCGAT
                                                                                                                                                                                                              GTCTCTATGC
                                                                                                                                                                                                                                         ATAAGAGGGG
                                                                                                                                                                                                                                                     TCATTACTCG
                                                                                                                                                                                                                                                                    AAGCTAGAGT
                                                                                                                                                                                                                                                                                              ATGAGCAGAT
                                                                                                                                                                                                                                                                                                                                                     GGATATTGGA
TAGGCGATAT
                                                                                                                         TAAATCTTGA
                                                                                                                                                                                   GATGGTACTG
                                                                                                                                                                                                TAGTATGGAA
                                                                                                                                                                                                                         TTGTAAAATA
                          GAAAGCCAAA
                                                                                 GAAACGAAGT
                                                                                               GCTACACACC
                                                                                                            TAGATTTTAG
                                                                                                                                                                                                                                                                                                                                        TACGATCCCA
                                                                                                                                                                                                                                                                                                                                                                  ACAAGACAAG
ATGCAGAGAA
              TATCATGTAA
                                        AGTGGAGAGA
                                                                                                                                                                                                                                                     GAAGGAAAAG
                                                                                                                                                                                                                                                                   AAAGAAACTC
                                                                                                                                                                                                                                                                               GTGAGAATAG
                                                                                                                                                                                                                                                                                                                         GGATACATAG
                          GCAATTTTTG
                                                      GAACTCGGGA
                                                                                               CTCAGGGAGA
                                                                                                           ATAGTATACC
                                                                                                                          CCCGATACTC
                                                                                                                                                      AGACAAAAGA
                                                                                                                                                                   GACTATAGAC
                                                                                                                                                                                              TACATCGAGT
                                                                                                                                                                                                                          GCTCTAGAAT
                                                                                                                                                                                                                                                                                              CTCGCAATAT
                                                                                                                                                                                                                                                                                                                                                      GCGGTACTTA
                                                                    TTATGGGATG
                                                                                 GCCTACGAAA
                                                                                                                                        AAGTTCTGCA
                                                                                                                                                                                  GCAAAAGCAA
                                                                                                                                                                                                             GACACTGATG
                                                                                                                                                                                                                                         GAAGGGTTTT
                                                                                                                                                                                                                                                                                                             GTAGCTGTTG
```

AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC CCG AAG GAG GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GCG GTA AGC GAA AAG GAC GCG CAG AAA AAG GGT CGT AAG TTC AAG CGT GAG TGG gg CTG GTA AAG ATC AAG AAA GTA ACC AAG ATG // GCA ACC GGT GGC CTG CAG

Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

FIGURE 17JJJ (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) 1200 1500 1260 1320 1560 1620 1680 1740 1800 1860 1920 2100 1020 1080 1140 1380 2040 1440 1980 480 840 960 540 900 AGCCTGGGAA AAAGAAAAG ACCAGAGAAG CATTTACGCT CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA CAAGCCTATT CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT ATTACTTGGA AAAACATAGA TCTTCCATAC CGAGCCCAAG TTTCGACTTG TGTATATGAA GGCAACTTAT ACTTAGGAAA TCAAAGAAGG CAATGTTTCT AGTAGGCCAC GTTAGAGGAA AATACTCCTT GGGAAGAAAG GCTTGAATAT TGAAATTGCA TGAAGAAGCT AGGTCCTCAC AATGGTAATT AAAGAGATAC ATATTTAGCG TGGACAACCT AATAGATGAA AGCTGAGGAA GGTTCTTCCA CCACTATTAG AGAAAAGTT TCTTGCCTTC GTGGGAAAAC TTATGGCTAT CCTCTACATT ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA TATCAGGGAG D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CACTAGAGGC GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA TITCAAGGIC AAGCACAGGG AACCITGIAG AGIGGIICII GGAGGAGAAA GTGAGGAAAT CTTGCCAATT ATGAAATTCC TGGAGAACCA GTTGAGAAA AGTTTCTCGG GAGAGAGATG ATAAAGAGAT TTCTCAGGAT GAAGAATACA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCTACGGATA ACGGAGATGT GGGCAATTCT CAAGATTAGT TCGCTCCTCA CTATAGAAAA GGTATGCAGT GAGATTGGAG TTACATGAGT ATAAGGCGAT TAAAGCCAGG TTAGACCATA TTCCATTTGC GGGGAAGAAG AGCTAAAGAT TCGCATTCCC TACTCGATGG AAGATGCAAA AAAAGGGGTT TAATTACCCA TGGGACATTT TTACTGCCTG GATTTAAAGT GACTGCTAGA ACCATTGGAA GAGATGGAAG GAATACGATA GGAGACTCAT GAAGTCAAGG CCAACATACA ATTCAGCTTT AAAGAGCCAG CCCTCGATTA AACTATGATA CCAAGTCTCT TTAAGACAAA AATGAAGGAA ACTCAAGATC GAAAAGTTTG CATAAATTCA AAGCTCCCTG TGGTTTAGAG ATAGTTAGGA TTTGGAGACA ATACTAAAAC CGATGGTCCA ATTAGCAATA GAATATTACA AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT CAAGATXXXC GCAAATTCTT GCTGAGAGCG ACGAAGAAGA GGAGTTAAAA AGCAAAGGTG GACGGCTGTA ACCTTGAGAG AGTTGCCAAA TCCAATGGAA TAAATCTTGA GGGATGCAAG AAAAAGCGAT AAAACTCTTA GTCTCTATGC AACTATCCCA AGCTGCTAAA TACGATCCCA AAAAGCACAA GTATGACGCA TGTAGAGAAG ACCGIGIGGA AACTITATIT GGAACAICCC CAGCAGTTGT GGACATCTTC ACCAATGGAG TACTTATAAT GATTAAATTA AATAAATCTC GCTACACA GTTGGATTCGTT TAGATTTTAG AGCCCTATAT AGGACATCCC TGGTTTTATA TAAGGAGTGT GGAGCTCGAA ATTCTTCGTT TAAAAGAAGT AATACAAAAG ATGAGCAGAT AACAAGACCA AAGATTGTGA GAATTGTTGA TAGGCGATAT AAGAATTCCT GATGGTACTG TACTTAGAGG AAGGCCTAAT CCCTCTATCA TATCAAGCGA ACATTATAGT AAAAACTTGG TAACAAGGAC TAGTATGGAA ATAAGAGGGG AAGCTAGAGT CAAAGAAACT ATGAAAATGA TTGTAAAATA TCATTACTCG AAGTTCTGCA AGACAAAAGA AAAGAAACTC GTGAGAATAG CTCGCAATAT GGATACATAG AGTGGAGAGA ATAGTATACC CCCGATACTC GACTATAGAC TACATCGAGT GCTCTAGAAT GAAGGAAAAG AGAGAACATC CTCATCGACA GCNATAGCNA AGTTATGCAG AAGGATCCTG ATGCAGAGAA TATCATGTAA GAACTCGGGA TTATGGGATG GCCTACGAAA CTCAGGGAGA GCAAAAGCAA GACACTGATG GTTGAGGTTG AAAAGGGCAG GCAATTTTG GAAGGGTTTT GTAGCTGTTG

FIGURE 17JJJ (CONT.)

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GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
                                                                    ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
```

ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC // TGA CTG CAG ATG CTG GAG AAG CAG AAA AAG TAC AAG GGT GGC AAG ACC GGC CGT TIC // GCA ACC GTA AAG

Figure 17KKK

KOD DNA POLYMERASE - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 71) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

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1200
                                                                                                                                                                                                                                                                                                                                                         1140
                                                                                                                                                                                                                                                                                                                                       1080
                                                                                                                                                                   540
                                                                                                                                                                                                                                                              840
                                                                                                                                                                                                                                                                                                                                                         GGCCAGAAGA
                                                                                                                                                                                                                                                                                                                                                                          GGAGAACATA
                                                                                                                                                                                                                                                              CGTTTATGAA
                                                                                                                                                                                                                                                                                                                                       CCTCAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                               CGGCCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                TICTGCAAGG ACTICCCAGG AITTAICCCG AGCCTGCTIG GAGACCTCCT AGAGGAGAGG
                   ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG
                                     TIGAACCCIA CIICIACGCC
                                                       ACGATICIGC CATIGAGGAA GICAAGAAGA TAACCGCCGA GAGGCACGGG
                                                                       ACGGITGIAA CGGITAAGCG GGITGAAAAG GITCAGAAGA AGITCCICGG GAGACCAGIT
                                                                                                                              GCTCGCCTTC
                                                                                                                                                                                                                                                                               AGCCTGGGAA
                                                                                                                                                                                                                                                                                                                                                                                            CGTCTCGCCG
                                                                                          GGACAAGATA
                                                                                                            CAAGCGCTAC
                                                                                                                                                                  GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC
                                                                                                                                                                                       TGTGAAGGAG
                                                                                                                                                                                                       CTATCTGAAA
                                                                                                                                                                                                                                             CTTCGATCTC
                                                                                                                                                                                                                                                                                                 GGTCACATAC
                                                                                                                                                                                                                                                                                                                    CGGCCAGTCC
                                                                                                                                                   CCTTATGATA
                                                                                                                                                                                                                         CGAGCCGAAG
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
                                                                                                                                                                                                                                                                                                                                     AGTGGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                              CCCCACAGGT
                                                                                                                                                                                     GAGGGAGATG ATAAAGCGCT TCCTCCGTGT
                                                                                                                                                                                                                                                                                                                   CTCGCTTAAT
                                                                                         CAGCGATAAG
                                                                                                            TACCCTTCGC
                                                                                                                              GGCGACGAGG AGCTGAAAT
                                                                                                                                                                                                                                                             CGCTTGAGGC
                                                                                                                                                                                                                                                                              GGAGAAGGIT TACGCIGAGG AAATAACCAC
                                                                                                                                                                                                                                                                                                 AAGATGCGAA
                                                                                                                                                                                                                                                                                                                                                       GGCCCCGAAC AAGCCCGATG AAAAGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                            TCACCCACAA
                                                                                                                                                   AGGGGCCAAT
                                                                                                                                                                                                                         GGGATGGAAG
                                                                                                                                                                                                                                           GACGGATACA
                                                                                                                                                                                                                                                                                                                                                                           GAGGGTTGTG
                                                                                                                                                                                                         TCGACTTCGC
                                                                                                                                                  GAGTTCGCCG
                                                                                                                                                                                                                                                                                                                                     AACCTCGTTG
                                                                                                                                                                                                         GGCGACAACT
                                                                                                                                                                                                                                                                                                 TACTCGATGG
                                                                                                                                                                                                                                                                                                                                                                                                              ACAGAGAAGG ATGCAAGGAA TATGACGTTG
                                     AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT
                                                                                          TACTCATCCG CAGGACXXXC
                                                                                                            TGACATCTAC GAGTACGACA
                                                                                                                                                                                                                         GCCCTCGGAA
                                                                                                                                                                                                                                           GTTTGCCGTC GAAGTGAAGG
                                                                                                                                                                                                                                                             CCCACATACA
                                                                                                                                                                                                                                                                                                                    TCCGATGGAG GCCCAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                            TCAATCATCA
                                                                                                                                                                                                                                                                                                                                                                           CTATGTAAAA GAGCCCGAGA
                                                                                                                                                                                                                                                                                                                                      CAGCACTGGC
                                                                                                                                                                                                                                                                                                                                                                                            CCTGTACCCC
                                                                                                                              GCCAATGGAA
                                                                                                                                                  TGAGGGCGAG
                                                                                                                                                                                                                                                             GATAAACCTG
                                                                                                                                                                                                         AACCTACAAC
                                                                                                                                                                                                                         AATAAACTTC
                                                                                                                                                                                                                                                                                                 AGTCGCCCGC
                                                                                          AACTCTACTT
                                                                                                            CAGCAGTTAT
                                                                                                                                                                                                                                                                                                                                                                           ATGAAGGAGG
                                                                                                                                                                                                                                                             TAAGACGGAC
                                                                                                                                                                                                                                                                                                  ACCTTGAGAG
                                                                                                                                                                                                                                                                                                                                                        GGAATGAGCT
                                                                                                                              AGGGATTAGT
                                                                                                                                                                   ACGAGGAAGG
                                                                                                                                                                                                          ACGLICICAL
                                                                                                                                                                                                                         AAAAGCTCGG
                                                                                                                                                                                                                                                                                                                   AGGAGTTCCT
                                                                                                                                                                                                                                                                                                                                      TCTCCCGCTC
                                                                                                                                                                                                                                                                                                                                                                                            ATTTAGATC
                                                                                                                                                  CTCTCTACCA
                                                                                                                                                                                       TCTCGACGGA
                                                                                                                                                                                                                                              TGGGCGACAG
                                                                                                                                                                                                                                                                                  GTCAGCCGAA
                                                                                            GAGGTCTGGA
                                                                                                                                                                                                                                                                                                                                     CTCTGGGACG
                                                                                                                                                                                                                                                                                                                                                                          CGGCAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                SATACGCTCA
                                                       CTCCTGAAGG
                                                                                                                                CTCATAGACA
                                                                                                                                                                  AGCTACGCCG
                                                                                                                                                                                                         AAAGACCCGG
                                                                                                                                                                                                                                                                                                  ACCGGCGAGA
                                                                                                                                                                                                                                                                                                                                                         GCCTATGAGA
                                                                                                                                                                                                                                                                                                                                                                                               GTGTACCTAG
                                                                                                            CGAGAGCATC
                                                                                                                                                   GACATTGAAA
                                                                                                                                                                                       GTTGACGTCG
                                                                                                                                                                                                                         AAGCGCTGTG
                                                                                                                                                                                                                                                                TATCCTGTGA
                                                                                                                                                                                                                                                                                                                    SAGCTTGGGA
                                                                                                                                                                                                                                              ATTCAGAGGA
                                                                                                                                                                                                                                                                                  GCCGTCTTCG
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FIGURE 17KKK (CONT.)

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1680
                                                                                    1740
                                                                                                   1800
                                                                                                                     1860
                                                                                                                                       1920
                                                                                                                                                       1980
                                                                                                                                                                       2040
                                                                                                                                                                                       2100
                                                                                                                                                                                                        2160
                                                   1620
                                                                                                                                                                                                      CGACGAGTTC
                                                                                                                                                                                                                                         CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG
                                                                  AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT
                                                                                  CGAGTACGAG
                                                                                                   AGACGAGGAA
GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT
                  CGGCTATGCA
                                                                                                                     GATAGCGAAA
                                                                                                                                       GAAGGCCGTG
                                                                                                                                                       GGAGAAGCTG
                                                                                                                                                                     TCCCCACGIT
                                                                                                                                                                                       GGTGATAAGC
                                                                                                                                                                                                                         TCTCCCAGCC
                                  AAGGGAGTAC
                                                   CTACAGCGAC
                 GATCCTGGCA AACAGCTACT ACGGTTACTA
                                  CGGCCTGGGG
                                                 TTAAGGTAAT
                                                                                  CTTCCGGGCG CGCTTGAGCT
                                                                                                   CTTCGTCACG AAGAAGAAGT ATGCGGTGAT
                                                                                                                     GTGAGGCGTG ACTGGAGCGA
                                                                                                                                                     CGAAAAGCTG AGCAAGTACG AGGTTCCGCC
                                                                                                                                                                      GAGGGATTTA AAGGACTACA AGGCAACCGG
                                                                                                                                                                                                                        CGACGCCGAG TACTACATTG AGAACCAGGT
                                                                                                                                     CTAAAGGACG GTGACGTCGA
                                                                                                                                                                                       GCCCTGGAAC
                                                                                                                                                                                                        CGATACCGTT
                                                                                                                                                                                                                                                          GITTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
                                                  AAGTACGGCT
                                  GGAGTGTGCA GAGAGCGTAA
                                                                                                                                                                                        CGCGAGAGGA GTCAAAATAC
                                                                                                                                                                                                        GGCGACAGGG
                                                   GATAGAGGAA
                                                                                    CAACGCCAAA
                                                                                                                     ACTTGAGATT
                                                                                                                                                                                                        TGGGAGGATA
                                                                                                                                       TGAAGCTTTG
                                                                                                                                                                                                                                         TTCTGAGAGC
    AGAAGAAGAT
                   GGGCCATCAA
                                   GGTACTGCAA
                                                   CCATCAAGGA
                                                                     TTTTGCCAC
                                                                                                    AACGCGGCTT
                                                                                                                      CAACGCGCGG
                                                                                                                                       CGAGGGTTCT
                                                                                                                                                       AAGAAGTTAC
                                                                                                                                                                       AGCAGATAAC
                                                                                                                                                                                        AGAGGTTGGC
                                                                                                                                                                                                        TCAAGGGCTC
                                                                                                                                                                                                                          AGCACAAGTA
                                                                                     TCAAGTATAT
                                                                  ACCGACGGAT
                                                                                                                                                                                                                                                            AGACAGGTTG
    CAGAAGATAA
                                                                                                       GGCTTCTACA
                                                                                                                                                                         GTGATCCACG
                                                                                                                                                                                                                          GACCCGACGA
                                                                                                                                                                                                                                            GTTGAGAGAA
                    TACAGGCAGA
                                    AGGCGCGCT
                                                   ATAACGATGA
                                                                                     ATGGAGTTCC
                                                                                                                      GGCAAGATAA
                                                                                                                                        GAGACGCAGG
                                                                                                                                                         AGGATAGTCA
                                                                                                                                                                                          GCCGTTGCCA
                                                                                                                                                                                                           TACATCGTGC
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GGC CTG GAA AAA GAG GTA GAC ATC TCC ATC TCC TTC ACC TAC GAG GAG GAA AAG GAC GCG CCG AAG GAG GTG GGC AAG ATG GGT GCG GTA AGC GGC GAA CAG AAA AAG // AAG CGT CTG CAG ATG CTG GAG AAG GGT GGC AAG ACC GGC GTA TGG AAG AAA ACC ATC AAG GCA

Figure 17LLL

Sso7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34) CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG TIC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC AIC ICC AAA AAG GAG AAG CAG CGT GTG TGG CIGGTA GTA AAG GGT GGC AAG ACC AAG AAA CAG ATG //GCA ACC ATC CTG

FIGURE 17LLL (CONT.)

1680 1140 1260 1380 1800 1980 2100 1020 1080 1200 1320 1440 1500 1620 1740 1860 2040 1560 //ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60 840 900 960 AAGGAAAACG GCGAGITITAA GAITGAGTAC GACCGGACTI TIGAACCCTA CTICIACGCC 120 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180 CGGCTATGCA TCCCCACGTT CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC AAGGGAGTAC GATAGCGAAA GGAGAAGCTG CGACGAGTTC TCTCCCAGCC CAGCGATAAG GGACAAGATA CGGCCAGTCC CCTCAGGAAG GGAGAACATA AAAGAAGGCT AGACGAGGAA GAAGGCCGTG CGCAAGGAAG ACCTGCGCTA CCAGAAGACG TACCCTTCGC CAAGCGCTAC CCTTATGATA CGTTTATGAA GGTCACATAC GGCCAGAAGA CGICICGCCG AGAGGAGAGG GCTCCTCGAT CTACAGCGAC CGAGTACGAG GCICGCCIIC TCTCCCCTAC TGTGAAGGAG CTATCTGAAA CGAGCCGAAG CTTCGATCTC AGCCTGGGAA CGGCCACCGC GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325 GATCCTGGCA AACAGCTACT ACGGTTACTA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AGGTTCCGCC AAGGACTACA AGGCAACCGG GCCGATGCTG AAACCGTCAA AAGAAGAAGT ATGCGGTGAT TGGGAGGATA GGCGACAGGG CGATACCGTT TACTACATIG AGAACCAGGI CGCTTGAGCT GTGAGGCGTG ACTGGAGCGA GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GCCAATGGAA GGCGACGAGG AGCTGAAAT TCCTCCGTGT TCGACTTCGC AAATAACCAC AAGATGCGAA CTCGCTTAAT CAGCACTGGC AACCTCGTTG AGTGGTTCCT CTATGTAAAA GAGCCCGAGA GAGGGTTGTG TCACCCACAA TATGACGITG CCCCACAGGI GAGACCTCCT TCGAGAGGAA TTAAGGTAAT CTAAAGGACG GTGACGTCGA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT AGAACGTGGA GGGATGGAAG GACGGATACA CGCTTGAGGC GGCCCCGAAC AAGCCCGATG AAAAGGAGCT AGTCGCCCGC TACTCGATGG GATAGAGGAA AAGTACGGCT CTTCCGGGCG AGCAAGTACG CCTGTACCCC TCAATCATCA TGACATCTAC GAGTACGACA AACCTACAAC GGCGACAACT TACGCTGAGG ATTTATCCCG AGCCTGCTTG ATTGACCCGA AACTCTACTT TACTCATCCG CAGGACXXXC GGCCAGGGTG ATAACTTGGA ATAAAGCGCT GCCCTCGGAA GAAGTGAAGG CCCACATACA TCCGATGGAG GCCCAGCTTT ATGCAAGGAA GAAGGCCACG CTTCGTCACG ACTIGAGATT CGAAAAGCTG CTTCGGTTAC AATACCTGGA GAGGGATTTA CGACGCCGAG GAGGGAGATG CAACGCCAAA TGAAGCTTTG AATAAACTTC GTTTGCCGTC GGAGAAGGTT GATAAACCTG ACTTCCCAGG ACAGAGAAGG AGAAGAAGAT CCATCAAGGA TTTTGCCAC AAAAGCTCGG ACCTTGAGAG AGGAGTTCCT ATTTAGATC GGGCCATCAA GGTACTGCAA TCAAGTATAT CAACGCGCGG AAGAAGTTAC TCAAGGGCTC AGCACAAGTA TTCTGAGAGC CGGTTAAGCG ACGITCICAL GTCAGCCGAA TCTCCCGCTC ATGAAGGAGG AACGCGGCTT AGCAGATAAC AGAGGTTGGC CAGCAGTTAT AGGGATTAGT CTCTCTACCA ACGAGGAAGG TCTCGACGGA TGGGCGACAG TAAGACGGAC GGAATGAGCT CGAGGGTTCT GGCTTCTACA AGGATAGTCA TACATCGIGC GACCCGACGA GATACGCTCA TTCTGCAAGG TACAGGCAGA GTGATCCACG GCCGTTGCCA GTTGAGAGAA GAGGTCTGGA AAAGACCCGG GAGCTTGGGA CTCTGGGACG GCCTATGAGA GTGTACCTAG CAGAAGATAA AGGGCGCGCT ACCGACGGAT GGCAAGATAA AGACAGGTTG ACGGTTGTAA CTCATAGACA AGCTACGCCG AAGCGCTGTG TATCCTGTGA GCCGTCTTCG CGGCAGAGCT ATAACGATGA ATGGAGTTCC GAGACGCAGG CGAGAGCATC GACATTGAAA GTTGACGTCG ATTCAGAGGA ACCGGCGAGA

Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 35) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 36) CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CGA, CGC, CGG, V93R MUTANT: XXX = AGA, AGG,

CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG GAG GTA GAC ATC TCC TAC AAA GGC GAA GAA AAA AAG CAG AAA AAG AAG TIC TGG GAG ggG GTA AAG CTG CAG ATG CTG GGC AAG ACC //GCA ACC GTA ATC AAG AAA GGT

1020 1140 1200 1260 1080 999 840 900 960 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG AGGTTTGTGG TACTCACAAC TCCGATAGTA TATATATGCT GAGACATGGA AAGGGAAGTT GGGCAAAATA CAAGCGTTAT CCTTGCCTTT AATAATGATT TTTGCCGTAT TGTTAAAGAA GTATCTCATA ACATCCCGAA AATCCACTTT TGAGGCAGTT TGCCGCTATA TGCTAGGGCA GCTGATAGGT GTATCTTTA AGAGTATAAA TTGACCCGAT CGAAAGAAA TTCAGCCCTA TATTGAGGAG ATAAAGGCAA TAAAGGGCGA AATTTTGGG TTGTTCAAGT GGGACAAAGA TCAAGGGTAG CAGAGGAAAT CAATGGAAGA AGCCAGAAAA ACGATGTTGC CAGCTATGCG TACCCTTTGC GGAGACGAGG AGCTTAAGCT GAATTTGGAA AGGGCGAGAT AAAATATCGA TTGATTTGCC CGTATACGCT ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA TCGTGGAGTG CTGATGAGGA CAATAATAGT CCATACTCGG CCTGGGAGGA TATGTAAAAG GACCCTCATT GTCAGGAAAA GAATATGACA GGCCAGAGTA ATCACATGGA GGGGACAATT GCTGTGGAAA GCCCAGTACT CCGAACAAAC TGTAAGAATT AAGATATAAA GAAGAAAATG AAATCCACAA CAAGACXXXC ATAAAGCGTT GTCTTAGGAA AACCTCCCAA AAATTAGGAG ACCGGCAACC CTGTACCCTT TTTATTCCCT AACTTACAAT AAGGACGATA AACCAAAAGC GAGATCAAGC AATAGAACTT TGACATTTAC TGAGGGAGAT AAGAGAAATG GAAAAAACTA ATACCCTTGA AAAAGAGGCC CTTTCCGGGC TGCAGTGAAA CGAGCATCCC TCCCATGGAG TGATAGTTTT TGAACTTGCA TTTCCGCAGT AGTICGGCTT GGGAGTTTAA ATGACTCCGC CAGCTGTGGT AGGGCTTGAT ATGAAGAAGA ATGTGATAAT AAAAGCTGGG AGAGGATGGG CAGTTGTGCG AAGAAAGCAT TCGGGAAGGA GGGACGTCTC ACGCGAGGAA GAACAACTTA TTTATTGGA TCTGCAAGGA GAGTGCTCGA AGCTCATTTT CGTTTTATCA TGTCCAATGA TTTTAGGAAA AAACGGGCAG SCAATGAGGC CTTCTCAAAG CCCAAGATTC TATGAAGCAG TGGGAAACAG STATCCCCAG AAAGAGAACG GTCGATGTTG AAAGACCCCG ACGTATGAGC CAAAGTGTAT AGGGTGGCAT SAAAATATCA GGATATAGGT AAAACTGTGA GAAGTCTGGA AGGGAACATC CTCATAGACA GATATTGAAA AGTTATGCCG GATCTTTCC CGGCGCTTAA

FIGURE 17MMM (CONT.)

2100 2160 1680 1740 1800 1860 1920 1980 2040 TGCAGTCATA GCTTGAGCTT TTGGAGTGAG AAGTGTTGAA AGCCATTGGC ACCGGGCACA AATTTTACTT CGGCTATATG GGTTCCACTT CGCATGGGGG TAAGGTTCTT ACTCATTAAA AAACCAAGTT TTTAAGGTAT AGGACTACAA TAAAAGTGAA TTGCTTGCAA ACAGCTATTA AACTCCAAAC TTCCAGGTCT TTTGTTACAA AAAAGCGCTA TAAGGAGAGA GAGGCTATAC TTAAAGAGGG CAAAATACAG GCGATAGGGT ACTACATAGA GAAAGGAGGA GAATGTGCTG AAAGCGTTAC ATAGAGGAAA AGTTCGGCTT AAAAGCCTGA CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325 ATACCCGGGG GAGAAAATAG AGGGATTTAA GCAAGAGGGA GATCCGGACT TTGGAAGTAG GGAAAGATAA TTTGGATACA AAACTACATA GATAAGAGAA ACTCGAAGCG GGCTATTAAA GTACTCGAAG TTATGCCACA GAGAGGATTC AAAGGTTTTA GCAGATTACC ACACAAGTAC AACAAGGGGC AGATGTTGTA AAGACTTGCC CAAAGGGAGC AGGAATTCCT AGACTCAGGC AAGTTGTTAG CGATAGCAAA ATCCTAGAAA TACTTAGGAT GCAGGATAAC ATAGGCAAAG TTATCCATGA AGGCAAGATG TAGAGATGAC CTGACGGCTT GCTTTTACTT ATATCGTTCT TTGCCGGCAG ATAGCTAAGG AAAGCTGTAG ACAGAATACG ATGCTCGATT GGGTATCCTA AGACACTACA AAGAAAGCCA GATGAAGAGG GAAAAGCTTG CCTCATGTCG GAGTATGAGG ATAATAAGCT TATGCGGACA

Figure 17NNN

Vent DNA POLYMERASE - Seo7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71) CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

600 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG AATAGAACTT GACCCTCATT TTCAGCCCTA TATATGCT TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA AATAATGATT AAGGGAAGTT GGGCAAAATA CAAGCGTTAT CCTTGCCTTT TTTGCCGTAT AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA GTATCTCATA AGTICGGCTI GICTIAGGAA GGGACAAAGA ACAICCCGAA AATCCACTTT TGAGGCAGTT AATTTTGGG CAGCTATGCG AACTTACAAT GGGGACAATT TTGATTTGCC TCAAGGGTAG CAGITGIGG AAGGACGAIA AACCICCCAA CGIAIACGCI TGACATTTAC GAATATGACA TACCCTTTGC TCCCATGGAG GGAGACGAGG AGCTTAAGCT AGGGCGAGAT AAAATATCGA GTCAGGAAAA GAATTTGGAA GCTGTGGAAA CAAGACXXXC ATCACATGGA GGCCAGAGTA TGCAGTGAAA CGAGCATCCC TGAGGGAGAT TGATAGTTTT CAGCTGTGGT AGGGCTTGAT AAAAGCTGGG GGGAGTTTAA ATGACTCCGC CGTTTTATCA ATGTGATAAT AGAGGATGGG GAGTGCTCGA AGCTCATTTT ATGAAGAAGA TGTCCAATGA CTTCTCAAAG AAAGAGAACG AAAGACCCCG AAAACTGTGA AGGGAACATC CTCATAGACA GATATTGAAA AGTTATGCCG GTCGATGTTG AAACGGGCAG CCCAAGATTC SATCTTTCC GAAGTCTGGA

FIGURE 17NNN (CONT.)

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1200
                                                                                                                                                  1440
                                                                                                                                                                 1500
                                                                                                                                                                                  1560
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                                                                                                                                                                                                                                                                                                                                     2100
                                                                1140
                                                                                                1260
                                                                                                                                 1380
                                                                                                                                                                                                                                                                                                                                    ACCGGGCCACA
                                                                                                               TCCGATAGTA
                                                                                                                                                                 CGGCTATATG
                                                                                                                                                                                 CGCATGGGGG
                                                                                                                                                                                                                                                   TGCAGTCATA
                                                                                                                                                                                                                                                                  TTGGAGTGAG
                                               GTATCTTTTA
                                                                                               TACTCACAAC
                                                                                                                                GGACTTAATT
                                                                                                                                                CGAAAAGAAA
                                                                                                                                                                                                 TAAGGTICTI
                                                                                                                                                                                                                                   GCTTGAGCTT
                                                                                                                                                                                                                                                                                   AAGTGTTGAA
                                                                                                                                                                                                                                                                                                                     AGCCATTGGC
                                                                                                                                                                                                                                                                                                                                                     AATTTACTT
                                                                                                                                                                                                                                                                                                                                                                     AAACCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                     TTTAAGGTAT
 TGCCGCTATA
                 TGCTAGGGCA
                                 GCTGATAGGT
                                                                AGAGTATAAA
                                                                                AGGTTTGTGG
                                                                                                                                                                                                                  ACTCATTAAA
                                                                                                                                                                                                                                                                                                    GGTTCCACTT
                                                               CTGATGAGGA
TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT
                                                                               AGCCAGAAAA
                                                                                                                                                                                                                                                                                                                    GCAGATTACC AGGGATTTAA AGGACTACAA
                                                                                                                                                                                                                                                                                                                                    AAGACTTGCC GCAAGAGGA TAAAAGTGAA
                 CAATGGAAGA
                                                                                               CAATAATAGT
                                                                                                               ACGATGTTGC
                                                                                                                                               GAAGAAATG AAATCCACAA TTGACCCGAT
                                                                                                                                                                 GGCTATTAAA TTGCTTGCAA ACAGCTATTA
                                                                                                                                                                                                                                                  GAGAGGATIC ITIGITACAA AAAAGCGCTA
                                                                                                                                                                                                                                                                  TAAGGAGAGA
                                                                                                                                                                                                                                                                                   TTAAAGAGGG
                                                                                                                                                                                                                                                                                                   GAGAAATAG CAAAATACAG
                                                                                                                                                                                                                                                                                                                                                    GCGATAGGGT
                                                                                                                                                                                                                                                                                                                                                                    ACTACATAGA
                                                                                                                                                                                                                                                                                                                                                                                    ACTCGAAGCG TTTGGATACA GAAAGGAGGA
                                 TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA
                                               TCGTGGAGTG
                                                                                                                                CCATACTCGG
                                                                                                                                                                                 GTACTCGAAG GAATGTGCTG AAAGCGTTAC
                                                                                                                                                                                                 GATAAGAGAA ATAGAGGAAA AGTTCGGCTT
                                                                                                                                                                                                                 AAAAGCCTGA
                                                                                                                                                                                                                                 AAACTACATA AACTCCAAAC TTCCAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                     CAAAGCICAA AACAAACCGG CITAGAIGCA IGGCICAAGA GG 2325 //
                                                                                                                                                                                                                  TIAIGCCACA AIACCCGGGG
                                                                                                                                                                                                                                                                  GCAGGATAAC AACAAGGGGC TTGGAAGTAG
                                                               TGAACTTGCA CCGAACAAAC
                                                                               CCTGGGAGGA TATGTAAAAG
                                                                                                                                                                                                                                                                                   GAGGCTATAC
                                                                                                                                                                                                                                                                                                                                                    GGAAAGATAA
                                               GAGATCAAGC ACCGGCAACC
                                                                                                 CIGIACCCIT
                                                                                                               TGTAAGAATT
                                                                                                                                                                                                                                                                                                                                                                    ATCCTAGAAA ACACAAGTAC GATCCGGACT
                 AAGAAAGCAT GAAAAAACTA GCCCAGTACT
                                                                                                                                TTTATTCCCT
                                                                                                                                                                                                                                                                                   AAAGGTTTTA
                                                                                                                                                                                                                                                                                                     AGATGTTGTA
                                                                                                                                                                                                                                                                                                                                                    CAAAGGGAGC
                                                                                               TTTCCGCAGT
                                                                                                               AAAAGAGGC
                                                                                                                                CTTTCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                     TACTTAGGAT
                                                                                               TTTATTTGGA
                                                                                                                                                                                                                                   AGGAATTCCT
                                                                                                                                                                                                                                                   GCTTTTACTT
                                                                                                                                                                                                                                                                                   AGACTCAGGC
                                                                                                                                                                                                                                                                                                                     TTATCCATGA
                                                                                                                                                                                                                                                                                                                                     CGATAGCAAA
                                                                                                                                                                                  AGGCAAGATG
                                                                                                                                                                                                                  CTGACGGCTT
                                                                                                                                                                                                                                                                                                    AAGTTGTTAG
                                                                ACGCGAGGAA
                                                                                                                ATACCCTTGA
                                                                                                                                                                                                 TAGAGATGAC
                                                                                                                                                                                                                                                                                                                                                    ATATCGTTCT
                                                 GGGACGICIC
                                                                                 GAACAACTTA
                                                                                                                                 TCTGCAAGGA
                                                                                                                                                  AAGATATAAA
                                                                                                                                                                   ATAGGCAAAG
               TGGGAAACAG
                                                                                                                                                                                                                                                                                                                   GAAAAGCTTG
  IATGAAGCAG
                                ACGIAIGAGC
                                                                                               GAAAATATCA
                                                                                                               GTATCCCCAG
                                                                                                                                                GCAATGAGGC
                                                                                                                                                                                  GGGTATCCTA
                                                                                                                                                                                                  AGACACTACA
                                                                                                                                                                                                                                                                                                                                    CCTCATGTCG
                                                                                                                                                                                                                                                                                                                                                                     ACAGAATACG
                                                                                                                                                                                                                                                                                                                                                                                     TTGCCGGCAG
                                                               AGGGTGGCAT
                                                                                                                                                                 ATGCTCGATT
                                                                                                                                                                                                                                  AAGAAAGCCA
                                                                                                                                                                                                                                                                   GATGAAGAGG
                                                                                                                                                                                                                                                                                   ATAGCTAAGG
                                                                                                                                                                                                                                                                                                   AAAGCTGTAG
                                                                                                                                                                                                                                                                                                                                                    ATAATAAGCT
                                               CAAAGIGIAT
                                                                                 CGGCGCTTAA
                                                                                                                                GGATATAGGT
                                                                                                                                                                                                                  TATGCGGACA
                                                                                                                                                                                                                                                   GAGTATGAGG
```

ggG CIG GAA AAA GAG GTA GAC ATC TCC ACC TAC GAC GAG GAA AAG GAC GCG CCG AAG GAG ATC TCC TTC TAC AAA GGC GAA GTG GGC AAG ATG GGT GCG GTA AGC CAG AAA AAG AAG CGT CGI TTC AAG GAG $^{\mathrm{TGG}}$ ACC GGC CIG // GCA ACC GTA AAG ATC AAG AAA GTA AAG CTG CAG ATG GGT GGC

Figure 17000

Deep Vent- Smod7 DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 38)

FIGURE 17000 (CONT.)

FOSSIBLE COLONS FOR ARGININE/ ACID)	GATTTTCAAG		GAGGCATGGG	GGATAAGATA	GAAGAGGTAC	r gcrcgcartr 420	TATAATGATA	TCTCCCGTAC	GATAAGGGAG	CTATCTAGTT	TGAGCCAAAG	CTTTGACCTC	AGTTTATGAG	GGCCTGGGAG	GGTAACGTAC	CGGCCAGCCC	CCTCAGGAAG	CGAGAGAAGG	CTGGGAGGGG	TAACGICTCA	GGTTGGGCAC	ATTGGATGAA	GAAGATGCTT	TTATGGGTAC	GGGGAGGGAA	CTTATACATA	AAAGAAGAAA	GCTTGAGTAC	GATAGATGAG	CGAAATAGCC	T TGAGGAGGCA 1920	TCCAGAAAAG	AGGTCCGCAC	CATGGTGATA	TGCAGAGGAG	GGTTTTACCT	GTGGCAGAA	2328
CGT (ALL GLUTAMIC		-	TAACCGCCGA	• -	_	AGCTCAAGTT	AGGGCCCAT	AAAAGATCGA	TCCTCAAGGT	TCGACCTTCC	GGGACGGTAG	GAAGGATACA	CCCTCGAGGC	•	AGGATGCAAA	_	AGTGGTACCT	AGAGGGAGTA	•	_	-	_	_	•	-	-	-	-	AGTATGCGTT	GGGACTGGAG	•	•	ACAAGGCTAT	_	GGGCTATCCT	TAGAAAATCA	AAGACCTCAG	AGAAG
CGC, CGG,	GATGGGAAGC	GACAGAAACT	GTTAGGAAGA	CAGGACXXXC	GAGTACGACA	GGCGATGAAG	GAGTTCGCGA	ATAACGTGGA	ATAAAGCGGT	GGCGATTCTT	CCCCTGGGAA	GAGATAAAGG	CCAACATACA	TACGCTCACG	TATTCAATGG	GCCCAGCTTT	AACTTGGTGG	AAGCCGGATG	AAGGAGCCGG	CCCTCGATAA	GAATACGATG	CCCAGCCTGC	TCTAAAGACC	GCAAACAGCT	GCAGAGAGCG	GAAAAGTTCG	GGGGCAAAAC	AAGCTCCCAG	ACGAAGAAGA	ATAGTCAGGA	ATCCTAAAGC	CTGAGCAAGT	CTTCACGAGT	GGAGTAAAGG	ATAAGCAAGA	GAGTATTACA	TACAGGAAAG	AACATCAAGA
, AGG, CGA,	CATCACCGAG	GGTTGAGTAC	GATTGATGAG	TGAACACCCT	TGACATCTTT	TCCAATGGAA	CGAAGGGGAG	AGCCAAAGTC	GAGGGAGATG	TACCTACAAC	GATAAAGCTA	GACAGCGGTG	GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG	TTCAACTGGC	GGCTCCAAAC	GGGATACGTT	GAGCCTGTAC	AGGGTGTAGG	GGGGTTTATC	GATGAAAGCT	CAAAATCCTG	TAAGGAGTGC	GGAACTGGAG	CACAATTCCT	TATAAACGCC	GIICIICGIG	GGGGCTTGAA	CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA	GTATGACGCT	GGCCTTTGGG	GGCATGGCTT
': XXX = AGA,	ACGCTGACTA	GCGAGTTTAA	ATGACTCGCA	GGCTGTACTT	CCGCAGTTAT	AAGGCCTAAT	CCCTCTATCA	ATGAGGAAGA	TTTCCAGCGA	ATGTTATAAT	AAAAGCTCGG	TTGGGGATAT	TTAGGAGAAC	GAAAGCCAAA	GACTGGAGAG	GGGAGTTCTT	TTTCTAGGTC	GGAATGAATT	GCTACGCTGG	TAGATTTCAG	TGAACAGGGA	AGGACTTCCC	TAAAAAGGAA	AACGGGCAAT	GTTGGTACTG	TCGTAAGGAA	GACTCTACGC	TCGTAGATTA	ACGTGAGAGG	TAATCACTAG	AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG	GGAAGCATAA	GAATATTAGA	CAGGTCTTAC
V93R MUTANT:			CTCCTCAAAG	GAGGTATGGA	AGAGAGCATT	CTAATAGACA	GACATAGAAA	AGCTATGCTG	GTCGAGGTAG	AAAGATCCCG	AAGAGGCCG	ATGCAGAGGC	TACCACGTGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA	CTGTGGGATG	GCCTACGAGA	CTAAGGGAGA	TIAGITICCC	CCGGATACGC	AAGTTCTGCA	AGGCAAGAAA	GATTACAGGC	GCAAAAGCCC	TATATAGAGT	GACACAGATG	GCCCTAGAGT	GAGGCCTTCT	GAAGGGAAGA	AAAGAAACCC	GTAAAGATAG	CTAGTTATTT	GTTGCCGTGG	GGGTACATAG	TTCGATCTCA	GCCGTTCTTA	ACTAAACAGA

FIGURE 17000 (CONT.)

Figure 17PPP

Ssod7 - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC

ひゅうしか かんかん かんかん しょく かんしゅうしゅう しょうしゅん しょうしゅん しょうしゅん しゅうしゅん かんしん しゅうしょ しょうしゅん しょうしゃん しょく しゃんしゃん しゃんしゃん しゃんしゃん しゃんしゃん しゃん しゃんしゃん しゃん	でんぴつでんじまんじ	ではなるでで出るで	びななけなけれなび	こる なつかかかける ない	9
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GAGTTTAA	AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT	GACAGAAACT	TTAGACCTTA	CATTIACGCT	120
TGACTCGCA	CICCICAAAG AIGACICGCA GAIIGAIGAG GITAGGAAGA IAACCGCCGA GAGGCAIGGG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AATTATAGA	AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GCTGTACTT	SAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
CGCAGTTAT	AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC	GAGTACGACA	TICCGIICGC	GAAGAGGTAC	360
AGGCCTAAT	CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
CCTCTATCA	GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
ATGAGGAAGA	AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
LTTCCAGCGA	GTCGAGGTAG TITCCAGCGA GAGGGAGAIG ATAAAGCGGI TCCTCAAGGI GATAAGGGAG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	009
LTGTTATAAT	AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	099
AAAAGCTCGG	AAGAGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
TTGGGGGATAT	ATGCAGAGGC TTGGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780

FIGURE 17PPP (CONT.)

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1320
                                                                                                                                                    1500
                                                                                                                                                                 1560
                                                                                                                                                                              1620
                                                                                                                                                                                             1680
                                                                                                                                                                                                                       1800
                                                                                                                                                                                                                                   1860
                                                                                                                                                                                                                                                  1920
                                                                                                                                                                                                                                                                1980
                                                                                                                                                                                                                                                                                         2100
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                                                                                                                                                                                                                                                                                                                                 2280
                                        1020
                                                      1080
                                                                                  1200
                                                                                                                         1380
                                                                                                                                       1440
                                                                                                                                                                                                           1740
                                                                                                                                                                                                                                                                             2040
                                                                                                                                                                                                                                                                                                                     2220
                                                                     1140
                                                                                               1260
GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG
              TACGCTCACG AGATAGCTGA GGCCTGGGAG
                            GGTAACGTAC
                                                                    CGAGAGAAGG
                                                                                              TAACGTCTCA
                                                                                                                                      GAAGATGCTT
                                                                                                                                                    TTATGGGTAC
                                                                                                                                                                 GGGGAGGGAA
                                                                                                                                                                              CTTATACATA
                                                                                                                                                                                             AAAGAAGAAA
                                                                                                                                                                                                           GCTTGAGTAC
                                                                                                                                                                                                                       GATAGATGAG
                                                                                                                                                                                                                                   CGAAATAGCC
                                                                                                                                                                                                                                                  TGAGGAGGCA
                                                                                                                                                                                                                                                               TCCAGAAAAG
                                                                                                                                                                                                                                                                            AGGTCCGCAC
                                                                                                                                                                                                                                                                                          CATGGTGATA
                                                                                                                                                                                                                                                                                                                     GGTTTTACCT
                                                                                                                                                                                                                                                                                                                                 GTGGCAGAAG
                                        CGGCCAGCCC
                                                      CCTCAGGAAG
                                                                                   CTGGGAGGGG
                                                                                                           GGTTGGGCAC
                                                                                                                         ATTGGATGAA
                                                                                                                                                                                                                                                                            CTTCACGAGT ACAAGGCTAT
                            TATTCAATGG AGGATGCAAA
                                        CAAGGTTAGT
                                                                                 AAGGAGCCGG AGAAAGGGCT
                                                                                              TAATCACCCA
                                                                                                                                                   ATTATGGGTA
                                                                                                                                                                 TTACGGCCTG
                                                                                                                                                                                            CCGAGGAGAT
                                                                                                                                                                                                                       AGTATGCGTT
                                                                                                                                                                                                                                   GGGACTGGAG
                                                                                                                                                                                                                                                               ACGAAATACC
                                                      TTCAACTGGC AACTTGGTGG AGTGGTACCT
                                                                    AAGCCGGATG AGAGGGAGTA
                                                                                                           TCGCCCCAGA
                                                                                                                         TCAAGAGGTT
                                                                                                                                      CAATCGAGAA
                                                                                                                                                                                                          GGCTGTTGGA
                                                                                                                                                                                                                                                  ATGGCAACGT
                                                                                                                                                                                                                                                                                          TGAGGCCTGG
                                                                                                                                                                                                                                                                                                                                  GGCCTTTGGG TACAGGAAAG AAGACCTCAG
                                                                                                                                                                                GGTTCAAAGT
                                                                                                                                                                                                                                                                                                       GGGCTATCCT
                                                                                                                                                                                                                                                                                                                      TAGAAAATCA
                                                                                                                                                                                                                                                                                                                                              ACTABACAGA CAGGICITAC GGCAIGGCII AACAICAAGA AGAAG IAA
                                                                                              CCCTCGATAA
                                                                                                                                     TCTAAAGACC
                                                                                                                                                    GCAAACAGCT
                                                                                                                                                                 GCAGAGAGCG
                                                                                                                                                                              GAAAAGTTCG
                                                                                                                                                                                                                        ACGAAGAAGA
                                                                                                                                                                                                                                    ATAGTCAGGA
                                                                                                                                                                                                                                                  ATCCTAAAGC
                                                                                                                                                                                                                                                               CTGAGCAAGT
                                                                                                                                                                                                                                                                                           GGAGTAAAGG
                                                                                                                                                                                                                                                                                                                     GAGTATTACA
                                                                                                                         CCCAGCCTGC
                                                                                                                                                                                                                                                                                                       ATAAGCAAGA
                                                                                                           GAATACGATG
                                                                                                                                                                                             GGGCCAAAAC
                                          GCCCAGCTTT
                                                                                                                                                                                                           AAGCTCCCAG
                                                                                                                                                                                                                        GTTCTTCGTG
                                                                                                                                                                                                                                    GGGGCTTGAA
                                                                                                                                                                                                                                                                                         AGCCGCTAGA
                                                                                                                                                                                                                                                                                                       AGACGGGCCA
                                         CCCAATGGAG
                                                                    GGCTCCAAAC
                                                                                  GGGATACGTT
                                                                                                                                      GATGAAAGCT
                                                                                                                                                    CAAAATCCTG
                                                                                                                                                                                                                                                  CCTAGAGGCT
                                                                                                                                                                                                                                                                            CACGAGGCCC
               GGAGAAAGTT
                             AGTTGCAAAG
                                                                                                                                                                 TAAGGAGTGC
                                                                                                                                                                                             CACAATTCCT
                                                                                                                                                                                                           TATAAACGCC
                                                                                                                                                                                                                                                               AACTGAAAAG
                                                                                                GAGCCTGTAC
                                                                                                           AGGGTGTAGG
                                                                                                                         GGGGTTTATC
                                                                                                                                                                               GGAACTGGAG
                                                                                                                                                                                                                                                                                                                     GTATGACGCT
                                                                                                            TGAACAGGGA
                                                                                                                                                                                                                        ACGTGAGAGG
                                                                                                                                                                                                                                    TAATCACTAG
                                                                                                                                                                                                                                                                            ACGAGCAGAT
                                                                                                                                                                                                                                                                                           CAAAAAGGTT
                                                                                                                                                                                                                                                                                                        TGCTGAGGGG
                                                                                                                                                                                                                                                                                                                                 GAATATTAGA
 TTAGGAGAAC
                                                                                                                                                    AACGGGCAAT
                                                                                                                                                                  GTTGGTACTG
                                                                                                                                                                                TCGTAAGGAA
                                                                                                                                                                                             GACTCTACGC
                                                                                                                                                                                                           TCGTAGATTA
                                                                                                                                                                                                                                                                TTAAGGAGGT
                                                                                                                                                                                                                                                                                                                     GGAAGCATAA
                             GACTGGAGAG
                                                                                                                                       TAAAAAGGAA
                                                                                                                                                                                                                                                  AAGCAAAAGT
               GAAAGCCAAA
                                           GGGAGTTCTT
                                                      TTTCTAGGTC
                                                                    GGAATGAATT
                                                                                   GCTACGCTGG
                                                                                               TAGATTTCAG
                                                                                                                         AGGACTTCCC
                                                                                                                                                                                                                        GAGGCTTCT
                                                                                                                                                    GATTACAGGC
                                                                                                                                                                                                                                     GAAGGGAAGA
                                                                                                                                                                                                                                                                            CTAGTTATT
                                                                                                                                                                                                                                                                                                       GGGTACATAG
                                                                                                                                                                                                                                                                                                                     TTCGATCTCA
                                                      CTGTGGGATG
                                                                                                           CCGGATACGC
                                                                                                                                       AGGCAAGAAA
                                                                                                                                                                  GCAAAAGCCC
                                                                                                                                                                                                          GCCCTAGAGT
                                                                                                                                                                                                                                                                GTAAAGATAG
                                                                                                                                                                                                                                                                                          GTTGCCGTGG
                                                                                                                                                                                                                                                                                                                                   GCCGTTCTTA
  TACCACGTGA
               GCAATCTTCG
                                          GAGCTCGGTA
                                                                    GCCTACGAGA
                                                                                   CTAAGGGAGA
                                                                                               TTAGTTTCCC
                                                                                                                         AAGTTCTGCA
                                                                                                                                                                                 TATATAGAGT
                                                                                                                                                                                             GACACAGATG
                                                                                                                                                                                                                                                  AAAGAAACCC
                             ACTGGAAAGG
```

Figure 17000

JDF-3 - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 71) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

CAGGTCTGTGGAGGTCTTGGGTCCTTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGGTCATCGACATCTACGAGTACGACATACCC ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT

FIGURE 17000 (CONT.)

TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGAGAATQGAGACGCTCTACCACGAGGGAGAGAGTTTGGAA асвесветвестасетсааввессвваесвевествтвевасаататсетвтатставастттсвтавтстста фотператсататсатсасссасаса в стопев CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGG<mark>GCG</mark>ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT GTTAAAATCCGGCCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACGACGAGGACATTCCCTTCGACGACTTCGACCCGACGAAGCACAAGTACGATG CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCGGGGTCGGGCTTGGCCG ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGAGACCGGCGAGGGGGCTTGAGAG **GGTCGCGCCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC** a teccaggecaaga tegtactecagggag tegceccaagag ceptacgg categggaagggag tacatcgaaatgg tcatcagagag cttgaggaaaag tttaaaag tcct GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGGCTTGAGATAGTCAGGCGCG ACTGGAGCGAGATAGCGAAGGAGACGCCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAA GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGCGTTTGGCCGAGGT GCTTCTTGAGGGTCGTTAAGGAGGAGCCCGGACGTGCTGATAACATACAAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAAGCGCTGTGAGAAGCTTGGCGTGTAGC a colticega accade con a companda de contracaca de como de contra de como de como de como de como de como de c CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC GTGGCTGAAGCCGAAGGGGAAGAAGAAG/

TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG CTG CAG ATG CTG GAG AAG CAG AAA AAG //GCA ACC GTA AAG ATC AAG AAA GTA GGT GGC AAG ACC

Figure 17RRR

Sso7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

GAG AAG CAG AAA AAG CTG CAG ATG CTG

FIGURE 17RRR (CONT.)

CAGGTCTGTGGAGGTCTTGGGTCCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGGTCATCGACATCTACGAGTACGACATACCC TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGGTGGAAGGTGAGGAAGGTTAAACTCATGTCCTTCGAGATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAA ACCTCCCGACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAGATCTACGCCGAGGAGATAGCCACGCCTGGGAGACCGGCGGGGGGCTTGAGAG GGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC CAGAAGATAAAGAGGAAGATGAAGCCAACTCTCGACCCGCTGGAGAATCTCCTTCGATTACAGGCAACGGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT SAACTCGAATACGAGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAAAAAGTACGCGGTCATCGACGAGGAGGGCCAAGATAACCACGCGCGGGGCTTGAGATAGTCAGGCGCG GTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGGACTTCGACCCGACGAGGAAGTACGATG CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC acgcgctcttaaggacgacttgccatcgaagtaaatcaaaaagataacgcggagagaggcacgggtagtcgttaaggttaagggcgcggagaagaggtgaagaaaaagttcctcgg GCTTCTTGAGGGTCGTTAAGGAGGAGCCCGGACGTGCTGATAACATACAAACGCGGCGACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGTAGCTTT **ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGTTGAGGAAAAGTTCGGTTTTAAAGTCCT** CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGGGGACGCTGAAAACAGTCAAAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAAATGCGGCCTTCTC **ACTGGAGGAGATAGCGAAGGAGGCGAGGCGAGGGGTTTTGGAGGCGATACTCAGGCACGTGAAGAGGCCGTCAGAATTTGTCAGGGAAGTCACCGAAAAGCTGAGCAA** TGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGGAGGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT GTGGCTGAAGCCGAAGGAAGAAGAAGTGA SEO. ID. NOS.

(cited from Belova et al. (2001) Proc. Natl. Acad. Sci 98: 6015-6020)

EIGURE 18

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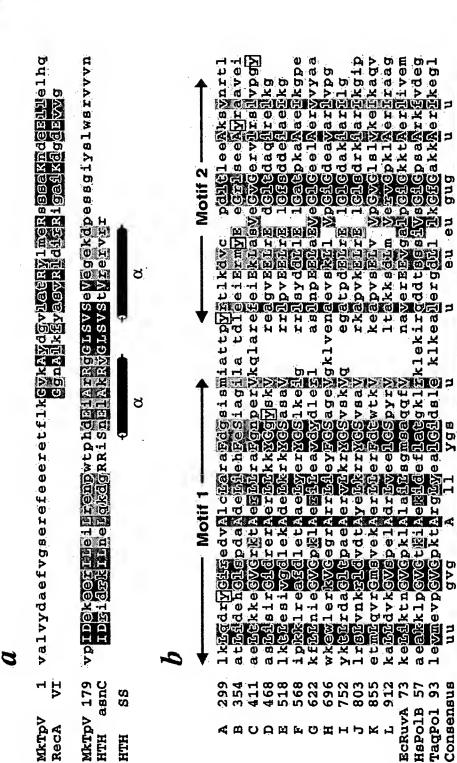
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 $\mathbf{\alpha}$

SS

HHH



174/186

FIGURE 19

SEQ ID NO: 120 Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGACATCTCCAA GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG CGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCCGAAGGAGC TGCTGCAGATGCTGGAGAAG CAGAAAAAG

SEQ ID NO: 121 The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQ MLEKQKK

SEQ ID NO: 122 The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG TGTCACTAGTCCCAAGGCcTGGAGGAGGCCCCCTGGCCCCGCCGGAAGGGGCC TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT GGCCGCCAGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC CCTGAGGGAAGGCCTTGGCCTCCGCCGGCGACGACCCCATGCTCCTCGCCTAC CTCCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGG GAGTGGACGAGGAGCGGGGGGGGCCCCCTTTCCGAGAGGCTCTTCGCC AACCTGTGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG GTGGAGAGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGC CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC GCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCG GGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA GACGGAGAAGACCGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCG CGAGGCCCACCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCT GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGCCG CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGCCAGGCTAAGTAGCTC CGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGC CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG ATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT TCCAGGAGGGCGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCC CCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG GGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTA CGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGAC CCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT GCGGGAGGCGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGA GAGGGCGGAGGCCGTGGCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCC CCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC CAAGGAGGCATTGATGGCCGCGGCGGAGGCGGCATCATCATCATCATTA A

SEQ ID NO: 123 The amino acid sequence of Sso7d-△Taq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA PKELLQMLEKQKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAA ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP SNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERPLS AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS QIELR VLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV LYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGRR RYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARMLL QVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDGR GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG TGTCACTAGTGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTG GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA GCCGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG CCTCAAGGAGGACGGGACGCGTGATCGTGGTCTTTGACGCCAAGGCCCCCT CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCACGCCAG AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT GGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCCTGGCCAGCCTGGC CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG ACCTTTACCAGCTCCTTTCCGACCGCATCCACCTCCACCCCGAGGGGTACCT CATCACCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGC CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG CATCGGGGAGAAGACGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG CCCTCCTCAAGAACCTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGG CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT GCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG GGCCTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG GAAAGCCCCAAGGCcCTGGAGGAGGCCCCCTGGCCCCGCCGGAAGGGGCCTTC GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG CCGCCGCAGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC TGAGGGAAGGCCTTGGCCTCCGCCGGCGACGACCCCATGCTCCTCGCCTACCT CCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA GTGGACGGAGGGGGGGGGGGCGCCCTTTCCGAGAGGCTCTTCGCCAA CCTGTGGGGGAGGCTTGAGGGGGAGGGGGGGCTCCTTTGGCTTTACCGGGAGGT GGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGCCT GGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCCG CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG GACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG ACGGAGAAGACCGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCGC GAGGCCCACCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCTG AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGCCGCC TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGCCAGGCTAAGTAGCTCCG ATCCCAACCTCCAGA. ACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT AGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC CAGGAGGGGGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCCCC CGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG GTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTACG AGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC

SEO ID NO: 125 The amino acid sequence of Sso7d-Tag fusion protein.

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA PKELLOMLEKOKKGGGVTSGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE PVQAVYGFAKSLLKALKEDGDAVIVVFDAKAPSFRHEAYGGYKAGRAPTPEDFPRQ LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSDR IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPGVKGIGEKTARKLL **EEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP** DRERLRAFLERLEFGSLLHEFGLLESPKALEEAPWPPPEGAFVGFVLSRKEPMWADL LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA YLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREV **ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILOYRELTKLKSTYIDPL** PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQIRJRRAFIAEEGWLLVA LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI NFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETL FGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGA RMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKE **GIDGRGGGGHHHHHH**

SEQ ID NO: 126 The DNA sequence encoding the Pfu-Sso7d fusion protein

ATGATTTTAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT TCAAAAAGAGAACGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAAACTTTATTTGGAACATCCCCAA GATGTTCCCACTATTAGAGAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC AATGGAGGGGAAGAAGACCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTCGACTTCCCATAT TTAGCGAAAAGGGCAGAAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG AAGAATACATTTCGACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA TACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGAAGGTA TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG CTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGAGCCAGAAAAGGGGTTGTGG GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC

TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT TTAGCAAATTCTTTCTACGGATATTATGGCTATGCAAAAGCAAGATGGTACTGTA AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT GGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG GAGTGAAATTGCAAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACA CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC CAATTATGAAATTCCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAAACTAGCT GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCAAA AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA CTTAGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAG ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAAAAAATCCGGTACCGGC GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC GACGAGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCC GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERH GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID LPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS EPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEI AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGN LVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFR ALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTK MKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIE LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYE GFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKETQARVLETILKHGDVEE AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKIKPG MVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKED LRYQKTRQVGLTSWLNIKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGKMIS FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-\Darageta fusion protein

atgattacga attcgacggt gaaggtaaag ttcaagtata agggtgaaga gaaagaagta gacacttcaa agataaagaa ggtttggaga gtaggcaaaa tggtgtcctt tacctatgac gacaatggta agacaggtag aggagctgta agcgagaaag atgctccaaa agaattatta gacatgttag caagagcaga aagagagaag aaaggcggcg gtgtcactag ccccaaggcc ctggaggagg ccccctggcc cccgccggaa ggggccttcg tgggctttgt gctttcccgc aaggageeca tgtgggeega tettetggee etggeegeeg eeaggggggg eegggteeae egggeeeeg ageettataa ageeeteagg gaeetgaagg aggegegggg gettetegee aaagacctga gcgttctggc cctgagggaa ggccttggcc tcccgcccgg cgacgacccc atgetecteg cetacetect ggaccettee aacaceaece eegaggggt ggeeeggege tacggcgggg agtggacgga ggaggcgggg gagcgggccg ccctttccga gaggctcttc gccaacctgt gggggaggct tgagggggag gagaggctcc tttggcttta ccgggaggtg gagaggeece ttteegetgt cetggeecac atggaggeea egggggtgeg cetggaegtg gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccgag gtetteegee tggeeggeea eeeetteaac etcaacteee gggaecaget ggaaagggte ctctttgacg agctagggct tcccgccatc ggcaagacgg agaagaccgg caagcgctcc accagegeeg cegteetgga ggeeeteege gaggeeeace ceategtgga gaagateetg cagtaccggg ageteaceaa getgaagage acetacattg acceettgee ggaceteate

SEQ ID NO: 129 The amino acid sequence of the Sac7d-△Taq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDA PKELLDMLARAEREKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL DPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERP LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLI HPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDY SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG VLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGR RRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARML LQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDG RGGGGHHHHHH

SEQ ID NO: 130 The DNA sequence encoding the PL-\Dangarage Tag fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA GAAAAAGAAAGCGCGCGCTGTCACTAGTGCCCAACCGTAAAGTTCAAGTACAA AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG GCAAGATGATCTCCTTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG CGGTAAGCGAAAAGGACGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG AAAAAGGCCGCGGTGTCACCAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC CCGCCGGAAGGGCCTTCGTGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG CCGATCTTCTGGCCCTGGCCGCCCAGGGGGGGCCCGGGTCCACCGGGCCCCCG AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG CATGCTCCTCGCCTACCTCCTGGACCCTTCCAACACCCCCCGAGGGGGTGGCC CGGCGCTACGGCGGGGGTGGACGGAGGAGGCGGGGGGGCCGCCCTTTCC GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT TGGCTTTACCGGGAGGTGGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGG CCACGGGGGTGCCCTGGACGTGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC AACCTCAACTCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTC CCGCCATCGCCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCC TGGAGGCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGG AGCTCACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC CAGGACGGCCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGCCAG GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG CAGAGGATCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAAC CTGATCCGGGTCTTCCAGGAGGGGGGGGGACATCCACACGGAGACCGCCAGCTGG

FIGURE 19 (CONT.)

ATGTTCGGCGTCCCCGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAG
ACCATCAACTTCGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCC
GGGTGAAGAGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCC
AGGGCACCGCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG
AGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGGGGGGCATCATC
ATCATCATCATTAA

SEQ ID NO: 131 The amino acid sequence of PL- \(\Delta Taq \) fusion protein

MITNSKKKKKKKKKKKKKKKKGGGVTSGATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTSPKALEEAPWPPPEG
AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV
EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAAD
LMKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHHH

SEQ ID NO: 132 PRIMER L71F 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQIDNO: 133 PRIMER L71R 5'-GCACAGCGGCTGGCTGAGGA-3'

SEQ ID NO: 134 PRIMER L18015F 15 5'-TGACGGAGGATAACGCCAGCAG-3'

SEQ ID NO: 135 PRIMER L23474R 5'-GAAAGACGA TGGGTCGCTAATACGC-3'

SEQ ID NO: 136 PRIMER L18015F 5'-TGACGGAGGATAAC GCCAGCAG-3'

SEQ ID NO: 137 PRIMER L29930R 5'-GGGGTTGGAGGTCAATGGGTTC-3'

SEQ ID NO: 138 PRIMER L3035OF 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 139 PRIMER L3512IR 30 5'- CACATGGTACAGCAAGCCTGGC-3'

SEQ ID NO: 140 PRIMER L2089F 5'-CCCGTATCTGCTGGGA TACTGGC-3'

SEQ IUD NO: 141 PRIMER L7112R 5'-CAGCGGTGCTGACTGAATCATGG-3'

SEQ ID NO: 142 PRIMER L3035OF 5 5'-CCTGCCTGCCGCTTCACGC-3'

SEQ ID NO: 143 PRIMER L40547R 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 PRIMER H-Amelo-Y 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 PRIMER H-Amelo-YR 5'-GCTTGAGGCCAACCATCAGAGC-3'

FIGURE 19 (CONT.)

SEQ ID NO: 146 Human beta-globin primer 536F 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 Human beta-globin primer 536R 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 Human beta-globin primer 1408R 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

Figure 20

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile

5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile 35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile 65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 245 250 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 260 265 270

FIGURE 20 (CONT.)

Tyr	Thr	Leu 275	Glu	Ala	Val	Tyr	Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys	Val 290	Tyr	Ala	Asp	Glu	Ile 295	Ala	Lys	Ala	Trp	Glu 300	Ser	Gly	Glu	Asn
Leu 305	Glu	Arg	Val	Ala	Lys 310	Tyr	Ser	Met	Glu	Asp 315	Ala	Lys	Ala	Thr	Tyr 320
Glu	Leu	Gly	Lys	Glu 325	Phe	Leu	Pro	Met	Glu 330	Ile	Gln	Leu	Ser	Arg 335	Leu
Val	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Phe	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Val	Ala
Pro	Asn 370	Lys	Pro	Ser	Glu	Glu 375	Glu	Tyr	Gln	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr 385	Thr	Gly	Gly	Phe	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Asn 400
Ile	Val	Tyr	Leu	Asp 405	Phe	Arg	Ala	Leu	Tyr 410	Pro	ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Leu	Glu	Gly	Cys	Lys 430	Asn	Tyr
Asp	Ile	Ala 435	Pro	Gln	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Ile	Pro	Gly
Phe	Ile 450	Pro	Ser	Leu	Leu	Gly 455	His	Leu	Leu	Glu	Glu 460	Arg	Gln	Lys	Ile
Lys 465	Thr	Lys	Met	Lys	Glu 470	Thr	Gln	Asp	Pro	Ile 475	Glu	Lys	Ile	Leu	Leu 480
Asp	Tyr	Arg	Gln	Lys 485	Ala	Ile	Lys	Leu	Leu 490	Ala	Asn	Ser	Phe	Tyr 495	Gly
Tyr	Tyr	Gly	Tyr 500	Ala	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser	Val	Thr 515	Ala	Trp	Gly	Arg	Lys 520	Tyr	Ile	Glu	Leu	Val 525	Trp	Lys	Glu
Leu	Glu 530	Glu	Lys	Phe	Gly	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly
Leu 545	Tyr	Ala	Thr	Ile	Pro 550	Gly	Gly	Glu	Ser	Glu 555	Glu	Ile	Lys	Lys	Lys 560
Ala	Leu	Glu	Phe	Val 565	Lys	Tyr	Ile	Asn	Ser 570	Lys	Leu	Pro	Gly	Leu 575	Leu

FIGURE 20 (CONT.)

Glu	Leu	Glu	Tyr 580	Glu	Gly	Phe	Tyr	Lys 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys	
Lys	Arg	Tyr 595	Ala	Val	Ile	Asp	Glu 600	Glu	Gly	Lys	Val	Ile 605	Thr	Arg	Gly	
Leu	Glu 610	Ile	Val	Arg	Arg	Asp 615	Trp	Ser	Glu	Ile	Ala 620	Lys	Glu	Thr	Gln	
Ala 625	Arg	Val	Leu	Glu	Thr 630	Ile	Leu	Lys	His	Gly 635	Asp	Val	Glu	Glu	Ala 640	
Val	Arg	Ile	Val	Lys 645	Glu	Val	Ile	Gln	Lys 650	Leu	Ala	Asn	Tyr	Glu 655	Ile	
Pro	Pro	Glu	Lys 660	Leu	Ala	Ile	Tyr	Glu 665	Gln	Ile	Thr	Arg	Pro 670	Leu	His	
Glu	Tyr	Lys 675	Ala	Ile	Gly	Pro	His 680	Val	Ala	Val	Ala	Lys 685	Lys	Leu	Ala	
Ala	Lys 690	Gly	Val	Lys	Ile	Lys 695	Pro	Gly	Met	Val	Ile 700	Gly	Tyr	Ile	Val	
Lev 705	Arg	Gly	Asp	Gly	Pro 710	Ile	Ser	Asn	Arg	Ala 715	Ile	Leu	Ala	Glu	Glu 720	
Tyr	Asp	Pro	Lys	Lys 725	His	Lys	Tyr	Asp	Ala 730	Glu	Tyr	Tyr	Ile	Glu 735	Asn	
Gln	Val	Leu	Pro 740	Ala	Val	Leu	Arg	Ile 745	Leu	Glu	Gly	Phe	Gly 750	Tyr	Arg	
Lys	Glu	Asp 755	Leu	Arg	Tyr	Gln	Lys 760	Thr	Arg	Gln	Val	Gly 765	Leu	Thr	Ser	
Trp	Leu 770	Asn	Ile	Lys	Lys	Ser 775										
PUF	IFIE	D TH	ERMO	STAB	LE P	YROC	OCCU	s FU	RIOS	JS DI	NA PO	OLYM	ERAS	ΕI		
NUC	LEOT	IDE :	SEQU	ENCE	(SE	Q ID	NO:	61)								
ccc	tggt	cct (gggt	ccaca	at a	tatg	ttct	t ac	tege	cttt	atga	aagaa	atc	CCCC	agtcgc	6(
tct	aacc	tgg (gtta	tagt	ga ca	aaat	cttc	c tc	cacca	accg	CCC	aaga	agg	ttati	ttctat	120
caa	ctct	aca (cctc	cccta	at t	tct	ctct	t at	gagat	tttt	taa	gtata	agt	tata	gagaag	180
gtt	ttat	act (ccaa	actga	ag ti	tagta	agata	a tg	tggg	gagc	ataa	atga	ttt	tagat	tgtgga	240
															aaatt	300
taa	gata	gag (catg	ataga	aa ci	tttt	agac	c ata	acati	ttac	gct	ette	tca (gggat	gattc	360
aaa	gatt	gaa (gaag	ttaa	ga aa	aata	acaa	a aa:	aaag	cat	ggaa	aaga	tta	taaa	aattgt	420

FIGURE 20 (CONT.)

tgatgtagag	aaggttgaga	aaaagtttct	cggcaagcct	attaccgtgt	ggaaacttta	480
tttggaacat	ccccaagatg	ttcccactat	tagagaaaaa	gttagagaac	atccagcagt	540
tgtggacatc	ttcgaatacg	atattccatt	tgcaaagaga	tacctcatcg	acaaaggcct	600
aataccaatg	gaggggaag	aagagctaaa	gattcttgcc	ttcgatatag	aaaccctcta	660
tcacgaagga	gaagagtttg	gaaaaggccc	aattataatg	attagttatg	cagatgaaaa	720
tgaagcaaag	gtgattactt	ggaaaaacat	agatcttcca	tacgttgagg	ttgtatcaag	780
cgagagagag	atgataaaga	gatttctcag	gattatcagg	gagaaggatc	ctgacattat	840
agttacttat	aatggagact	cattcgactt	cccatattta	gcgaaaaggg	cagaaaaact	900
tgggattaaa	ttaaccattg	gaagagatgg	aagcgagccc	aagatgcaga	gaataggcga	960
tatgacggct	gtagaagtca	agggaagaat	acatttcgac	ttgtatcatg	taataacaag	1020
gacaataaat	ctcccaacat	acacactaga	ggctgtatat	gaagcaattt	ttggaaagcc	1080
aaaggagaag	gtatacgccg	acgagatagc	aaaagcctgg	gaaagtggag	agaaccttga	1140
gagagttgcc	aaatactcga	tggaagatgc	aaaggcaact	tatgaactcg	ggaaagaatt	1200
ccttccaatg	gaaattcagc	tttcaagatt	agttggacaa	cctttatggg	atgtttcaag	1260
gtcaagcaca	gggaacct t g	tagagtggtt	cttacttagg	aaagcctacg	aaagaaacga	1320
agtagctcca	aacaagccaa	gtgaagagga	gtatcaaaga	aggctcaggg	agagctacac	1380
aggtggattc	gttaaagagc	cagaaaaggg	gttgtgggaa	aacatagtat	acctagattt	1440
tagagcccta	tatccctcga	ttataattac	ccacaatgtt	tctcccgata	ctctaaatct	1500
tgagggatgc	aagaactatg	atatcgctcc	tcaagtaggc	cacaagttct	gcaaggacat	1560
ccctggtttt	ataccaagtc	tcttgggaca	tttgttagag	gaaagacaaa	agattaagac	1620
aaaaatgaag	gaaactcaag	atcctataga	aaaaatactc	cttgactata	gacaaaaagc	1680
gataaaactc	ttagcaaatt	ctttctacgg	atattatggc	tatgcaaaag	caagatggta	1740
ctgtaaggag	tgtgctgaga	gcgttactgc	ctggggaaga	aagtacatcg	agttagtatg	1800
gaaggagctc	gaagaaaagt	ttggatttaa	agtcctctac	attgacactg	atggtctcta	1860
tgcaactatc	ccaggaggag	aaagtgagga	aataaagaaa	aaggctctag	aatttgtaaa	1920
atacataaat	tcaaagctcc	ctggactgct	agagcttgaa	tatgaagggt	tttataagag	1980
gggattcttc	gttacgaaga	agaggtatgc	agtaatagat	gaagaaggaa	aagtcattac	2040
tcgtggttta	gagatagtta	ggagagattg	gagtgaaatt	gcaaaagaaa	ctcaagctag	2100
agttttggag	acaatactaa	aacacggaga	tgttgaagaa	gctgtgagaa	tagtaaaaga	2160

REPLACEMENT SHEET FIGURE 20 (CONT.)

agtaatacaa	aagcttgcca	attatgaaat	tccaccagag	aagctcgcaa	tatatgagca	2220
gataacaaga	ccattacatg	agtataaggc	gataggtcct	cacgtagctg	ttgcaaagaa	2280
actagctgct	aaaggagtta	aaataaagcc	aggaatggta	attggataca	tagtacttag	2340
aggcgatggt	ccaattagca	atagggcaat	tctagctgag	gaatacgatc	ccaaaaagca	2400
caagtatgac	gcagaatatt	acattgagaa	ccaggttctt	ccagcggtac	ttaggatatt	2460
ggagggattt	ggatacagaa	aggaagacct	cagataccaa	aagacaagac	aagtcggcct	2520
aacttcctgg	cttaacatta	aaaaatccta	gaaaagcgat	agatatcaac	ttttattctt	2580
tctaaccttt	ttctatgaaa	gaagaactga	gcaggaatta	ccagttcttc	cgttatttta	2640
tgggtaatta	aaaacccatg	ctcttgggag	aatcttcgaa	taaaatccct	aacttcaggc	2700
tttgctaagt	gaatagaata	aacaacatca	ctcacttcaa	acgccttcgt	tagaaatggt	2760
ctatctgcat	gcttctctgg	ctcggaanng	gaggattcat	aacaacagta	tcaacattct	2820
cagagaattg	agaaacatca	gaaactttga	cttctacaac	atttctaact	ttgcaactct	2880
tcaagatttt	ctaaaagaat	tttaacggcc	tcctcgtcaa	tttcgacgac	gtagatcttt	2940
tttgctccaa	gcagagccgc	tccaatggat	aacacccctg	ttcccgcacc	caagtccgct	3000
acaattttt	ccttgtatct	cctaatgtat	aagcaagcca	aaggagagta	gatgctacct	3060
ttccgggagt	tttgtattgc	tctagccaag	gtttgggatt	tttgaatcct	ttaactctgg	3120
aaagtataat	ttcaagctcc	ttcttcttca	tgacagatga	aaaattgttt	tgtctctttt	3180
taacttttác	agaaataact	gtctcaaatt	atgacaactc	ttgacatttt	tacttcatta	3240
ccagggtaat	gtttttaagt	atgaaatttt	tctttcatag	aggaggnnnn	nngtcctctc	3300
ctcgatttcc	ttggttgtgc	tccatatgat	aagcttccaa	agtgggtgtt	cagactttta	3360
gacactcaaa	taccagacga	caatggtgtg	ctcactcaag	ccccatatgg	gttgagaaaa	3420
gtagaagcgg	cactactcag	atgcttcccc	aggaatgagg	ttgttgtagc	tentecenga	3480
aagattgaga	tgttcttgg					3499